

**FIG. 1A**

AGGGGCGCCGTGCGTGCGGGGAGCTGGAAGCCTCGAGCAGCCGGCGCCTTCT  
GGCTGCCCGG -120

CTGGCCCCGGGGCCCATATGGCTTGAAGAGCCCGTGCCACCCAGTGGCCCCCACTGCCCA

1	Met	Asp	Pro	Leu	Asn	Leu	Ser	Trp	Tyr	Asp	Asp	Leu	Glu	Arg
	ATG	GAT	CCA	CTG	AAC	CTG	TCC	TGG	TAC	GAT	GAC	CTG	GAG	AGG
	1				*					10				-1

Gln	Asn	Trp	Ser	Arg	Pro	Phe	Asn	Gly	Ser	Glu	Gly	Lys	Ala	Asp	30
CAG	AAC	TGG	AGC	CGG	CCC	TTC	AAT	GGG	TCA	GAA	GGG	AAG	GCA	GAC	90

Arg	Pro	His	Tyr	Asn	Tyr	Tyr	Ala	Met	Leu	Leu	Thr	Leu	Ile	90
AGG	CCC	CAC	TAC	AAC	TAC	TAT	GCC	ATG	CTG	CTC	ACC	CTC	CTC	
									40					

[illegible]

Arg	Glu	Lys	Ala	Leu	Gln	Thr	Thr	Thr	Asn	Tyr	Leu	Ile	Val	Ser	
GCA	GAG	AAG	GCT	TTG	CAG	ACC	ACC	ACC	AAC	TAC	TTG	ATA	GTC	AGC	
															70
Leu	Ala	Val	Ala	Asp	Leu	Leu	Val	Ala	Thr	Leu	Val	Met	Pro	Trp	90
CTT	GCT	GTG	GCT	GAT	CTT	CTG	GTG	GCC	ACA	CTG	GTA	ATG	CCG	TGG	
															270
Val	Val	Tyr	Leu	Glu	Val	Val	Gly	Glu	Trp	Lys	Phe	Ser	Arg	Ile	
GTT	GTC	TAC	CTG	GAG	GTG	GTG	GGT	GAG	TGG	AAA	TTC	AGC	AGG	ATT	
															100
His	Cys	Asp	Ile	Phe	Val	Thr	Leu	Asp	Val	Met	Met	Cys	Thr	Ala	120
CAC	TGT	GAC	ATC	TTT	GTC	ACT	CTG	GAT	GTC	ATG	ATG	TGC	ACA	GCA	
															360
Ser	Ile	Leu	Asn	Leu	Cys	Ala	Ile	Ser	Ile	Asp	Arg	Tyr	Thr	Ala	
AGC	ATC	CTG	AAC	CTG	TGT	GCC	ATC	AGC	ATT	GAC	AGG	TAC	ACA	GCT	
															130
Val	Ala	Met	Pro	Met	Leu	Tyr	Asn	Thr	Arg	Tyr	Ser	Ser	Lys	Arg	150
GTG	GCA	ATG	CCC	ATG	CTG	TAT	AAC	ACA	CGC	TAC	AGC	TCC	AAG	CGC	
															450

FIG. 1B

Arg	Val	Thr	Val	Met	Ile	Ala	Ile	Val	Trp	Val	Leu	Ser	Phe	Thr
CGA	GTT	ACT	GTC	ATG	ATT	GCC	ATT	GTC	TGG	GTC	CTG	TCC	TTC	ACC
160														
Ile	Ser	Cys	Pro	Leu	Leu	Phe	Gly	Leu	Asn	Asn	Thr	Asp	Gln	Asn
ATC	TCC	TGC	CCA	CTG	CTC	TTC	GGA	CTC	AAC	AAT	ACA	GAC	CAG	AAT
170														
Glu	Cys	Ile	Ile	Ala	Asn	Pro	Ala	Phe	Val	Val	Tyr	Ser	Ser	Ile
GAG	TGT	ATC	ATT	GCC	AAC	CCT	GCC	TTT	GTG	GTC	TAC	TCC	TCC	ATT
190														
Val	Ser	Phe	Tyr	Val	Pro	Phe	Ile	Val	Thr	Leu	Leu	Val	Tyr	Ile
GTC	TCA	TTC	TAC	GTG	CCC	TTC	ATC	GTC	ACT	CTG	CTG	GTC	TAT	ATC
200														
Lys	Ile	Tyr	Ile	Val	Leu	Arg	Lys	Arg	Arg	Lys	Arg	Val	Asn	Thr
AAA	ATC	TAC	ATC	GTC	CTC	CGG	AAG	CGC	CGG	AAG	CGG	GTC	AAC	ACC
220														
Lys	Arg	Ser	Ser	Arg	Ala	Phe	Arg	Ala	Asn	Leu	Lys	Thr	Pro	Leu
AAG	CGC	AGC	AGT	CGA	GCT	TTC	AGA	GCC	AAC	CTG	AAG	ACA	CCA	CTC
230														

FIG. 1C

Lys Asp Ala Ala Arg Arg Ala Gln Glu Leu	250	Glu Met Glu Met Leu
AAG GAT GCT GCC CGC CGA GCT CAG GAG CTG		GAA ATG GAG ATG CTG
Ser Ser Thr Ser Pro Pro Glu Arg Thr Arg	260	Tyr Ser Pro Ile Pro
TCA AGC ACC AGC CCC CCA GAG AGG ACC		TAT AGC CCC ATC CCT
Pro Ser His His Gln Leu Thr Leu Pro Asp	280	Pro Ser His His Gly
CCC AGT CAC CAC CAG CTC ACT CTC CCT GAT		CCA TCC CAC CAC GGC
Leu His Ser Asn Pro Pro Asp Ser Pro Ala	290	Lys Pro Gly Lys Asn Gly
CTA CAT AGC AAC CCT GAC GAC AGT CCT GCC		AAA CCA GAG AAG AAT GGG
His Ala Lys Ile Val Asn Pro Arg Ile Ala	310	Lys Phe Phe Glu Ile
CAC GCC AAG ATT GTC AAT CCC AGG ATT GCC		AAG TTC TTT GAG ATC
Gln Thr Met Pro Asn Gly Lys Thr Arg Thr	320	Ser Leu Lys Thr Met
CAG ACC ATG CCC AAT GGC AAA ACC CGG ACC		TCC CTT AAG ACG ATG
		990

FIG. 1D

Ser Arg Arg Lys Leu Ser Gln Gln Lys Glu Lys Lys Ala Thr Gln	340
AGC CGC AGA AAG CTC TCC CAG CAG AAG GAG GAG AAA GCC ACT CAG	
Met Leu Ala Ile Val Leu Gly Val Phe Ile Ile Cys Trp Leu Pro	360
ATG CTT GCC ATT GTT CTC CTC GGT GTG TTC ATC ATC TGC TGC CTG CCC	
Phe Phe Ile Thr His Ile Leu Asn Ile His Cys Asp Cys Asn Ile	370
TTC TTC ATC ACG CAC ATC ATC CTG AAT ATA CAC TGT GAT TGC AAC ATC	1080
Pro Pro Val Leu Tyr Ser Ala Phe Thr Trp Leu Gly Tyr Val Asn	390
CCA CCA GTC CTC TAC AGC AGC GCC TTC ACA TGG CTG GGC TAT GTC AAC	1170
Ser Ala Val Asn Pro Ile Ile Tyr Thr Thr Phe Asn Ile Glu Phe	400
AGT GCC GTC AAC CCC ATC ATC ATC TAC TAC ACC ACC TTC AAC ATC GAG TTC	
Arg Lys Ala Phe Met Lys Ile Leu His Cys	410
CGC AAG GCC TTC ATG AAG ATC -TTG CAC TGC TGAGTCTGCCCCCTTGCCCTG	1264

FIG. 1E

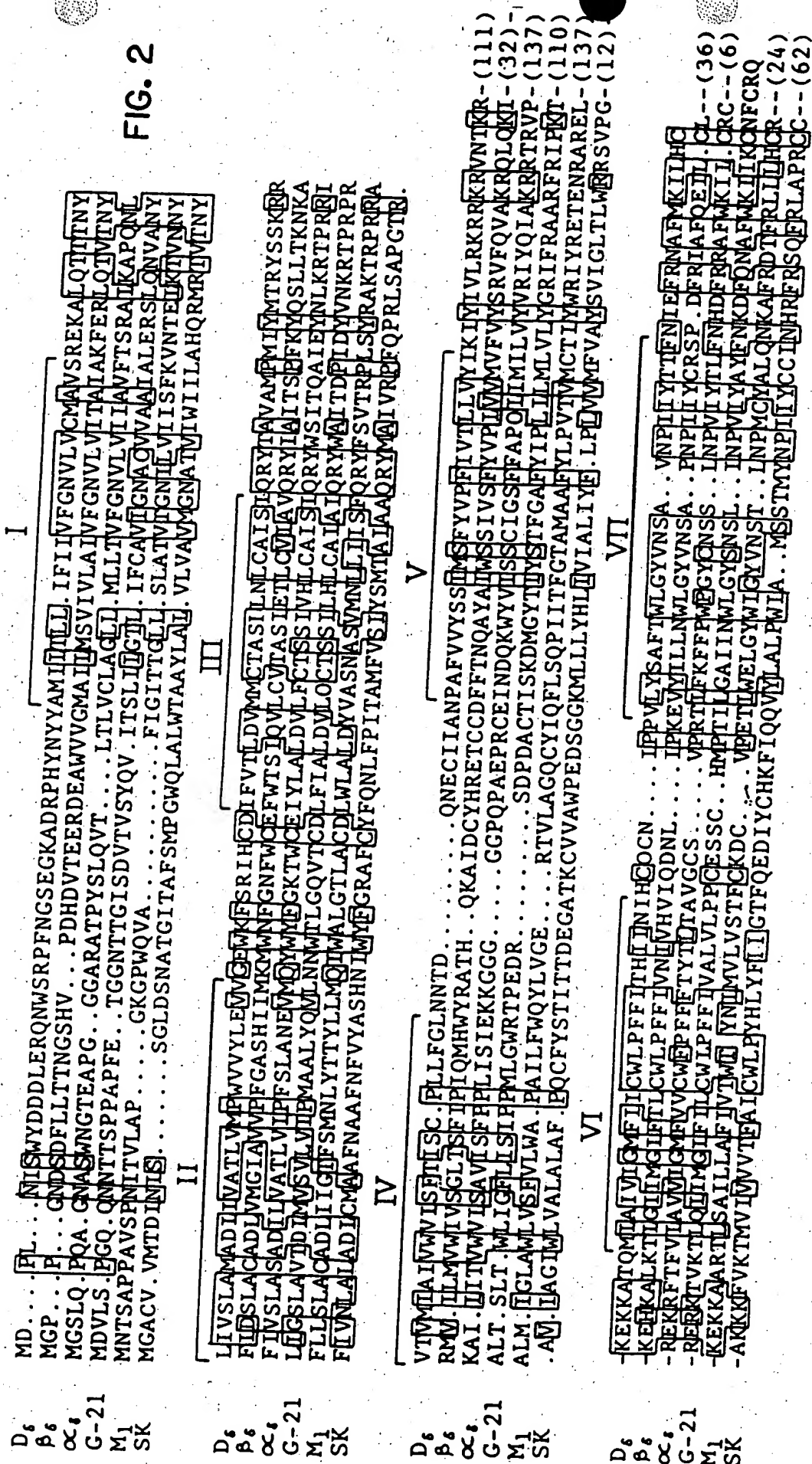
CACAGAGCTGCTTCCCACCTCCCTGCCCTATGCAGGCCAGACCTCATCCCTGCAAGCTG  
TGGCAGAAAGGCCAGATGAACCTTGGCCTTCTCTCGACCCCTGCAGGCCCTGCAGTGTTA  
GCTTGGCTCGATGCCCCCTCTCTGCCCACACACCCCTCATCCTGCCAGGGTAGGGCCAGGG 1383  
AGACTGGTATCTTACCAGCTCTGGGGTTGGACCCATGGCTCAGGGCAGCTCACAGAGTGC  
CCCTCTCATATCCAGACCCCTGTCTCCTTGGCACCAAGATGCAGCGGCCCTTCCTTGACC 1502  
TTCCTCTTGGGCACAGAACTAGCTCAGTGGTCGAGCACACCCCTGATCGCTGGCTTGCCC  
TGGCCCTTGCTTGCCCTGTGCCGATCAGGTGGTGGAGGAGCGACACGTTCTTACTTT 1621  
ATAGGAACCACATAGGAAAGCAGGGAACACGCCCAAGTCTCCAGGCACATCAGTGTCAAG 1740  
AGACACATAAACACCAGGTAGCTCCATGGACCCAGAGAAACTGAGGCTGAAAAATC  
TGTTTCCACTCCAACCTAGTGTGAGTCCCTACTTTTCATAGCCATGGGTATTACTATG 1859

FIG. 1F

TCCTACCTTGTTATAGTATCCCATGGGGTTTCTGTACCATTTGGGGGAAACAACACTCTA  
 ATCCTCAAGGGCCCCAAGAGAAATCTGTAAAGAGAAAAATAGGCTGATCTCCCTCTACTCT  
 CCAATCCACTCCACCACTTCTTGATATACCTTGGATGTATCCATTCTTCACAGCAAAATG 1978  
 CTGGCCAGTCAGGCCCTTGGACCAGTGTGGAGTTGAAGCTGGATGTGGTAACTTGGGGCT  
 CTTTGGGCTGGGGGGTGTAAACATCGTCTCTCTTCCATATCTCTTCCCTTCCCAGTG 2097  
 CCTCTGCCCTAGAAGAGGCTGTGGATGGGCTGCTGGGACTGCTGATACCATTTGGGCCCTGG  
 CCCTGAATGAGGAGGGGAAGCTGCAGTTTGGAGGGTCTGCGGATCCAACCTCTGTAAACAT 2216  
 CACTATACCTGTACCAAACTAATAAAACCTTGACAAGAGTCAAAAAAAA 2317

FIG. 1G

FIG. 2



D<sub>6</sub>  
β<sub>6</sub>  
α<sub>6</sub>  
G-21  
M<sub>1</sub>  
SK

D<sub>6</sub>  
β<sub>6</sub>  
α<sub>6</sub>  
G-21  
M<sub>1</sub>  
SK

D<sub>6</sub>  
β<sub>6</sub>  
α<sub>6</sub>  
G-21  
M<sub>1</sub>  
SK

D<sub>6</sub>  
β<sub>6</sub>  
α<sub>6</sub>  
G-21  
M<sub>1</sub>  
SK



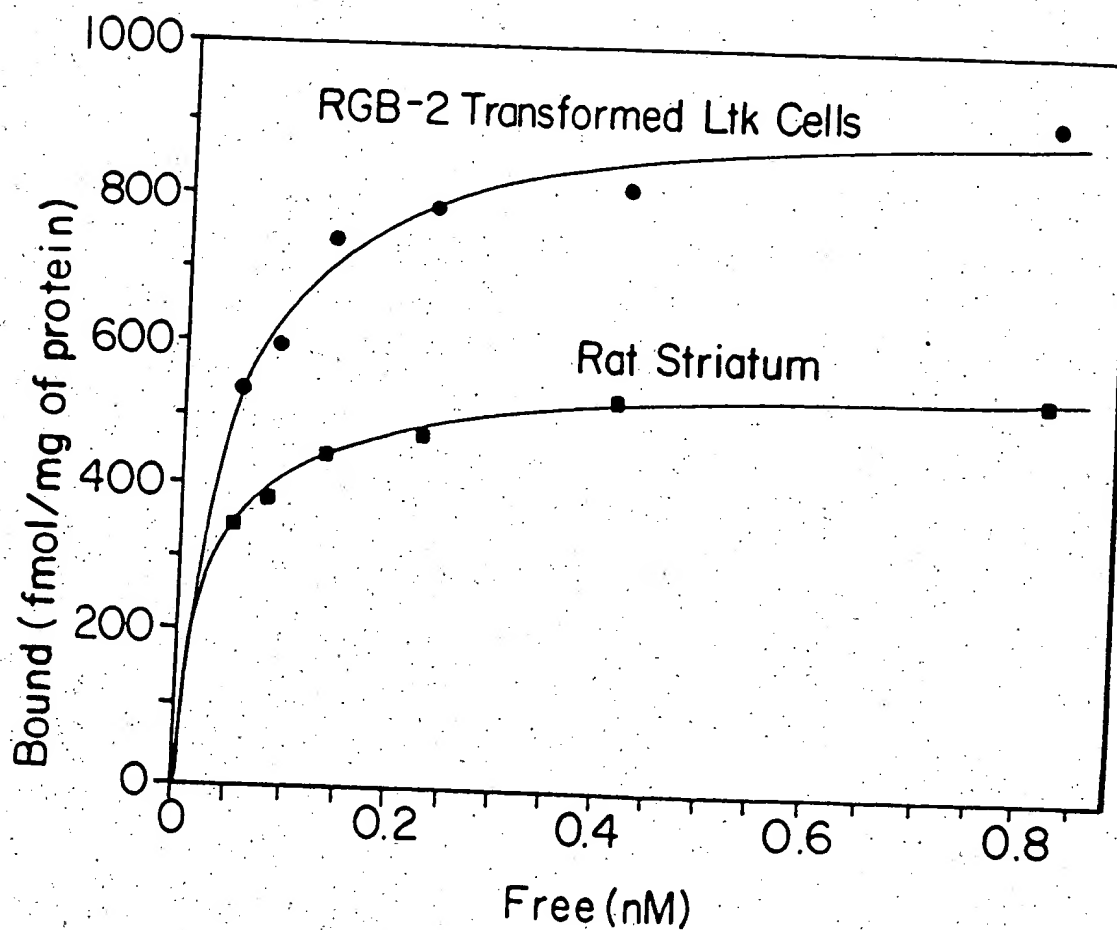


FIG. 4A-1

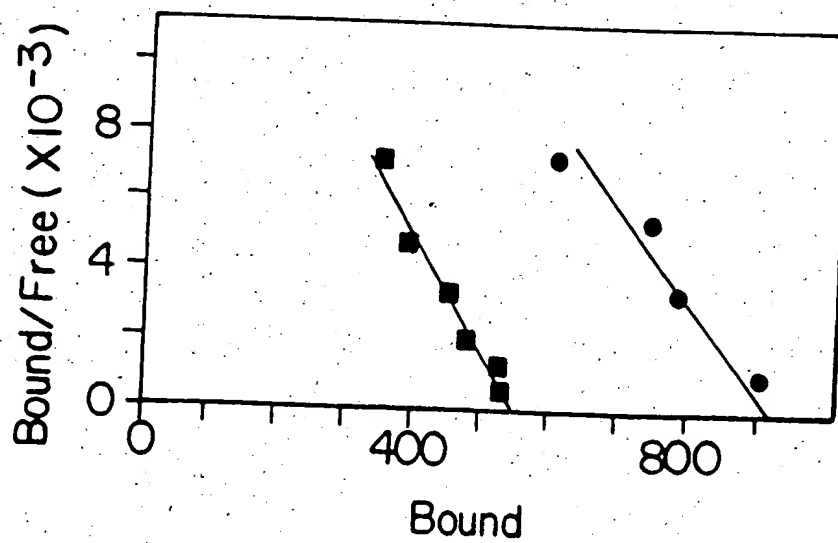
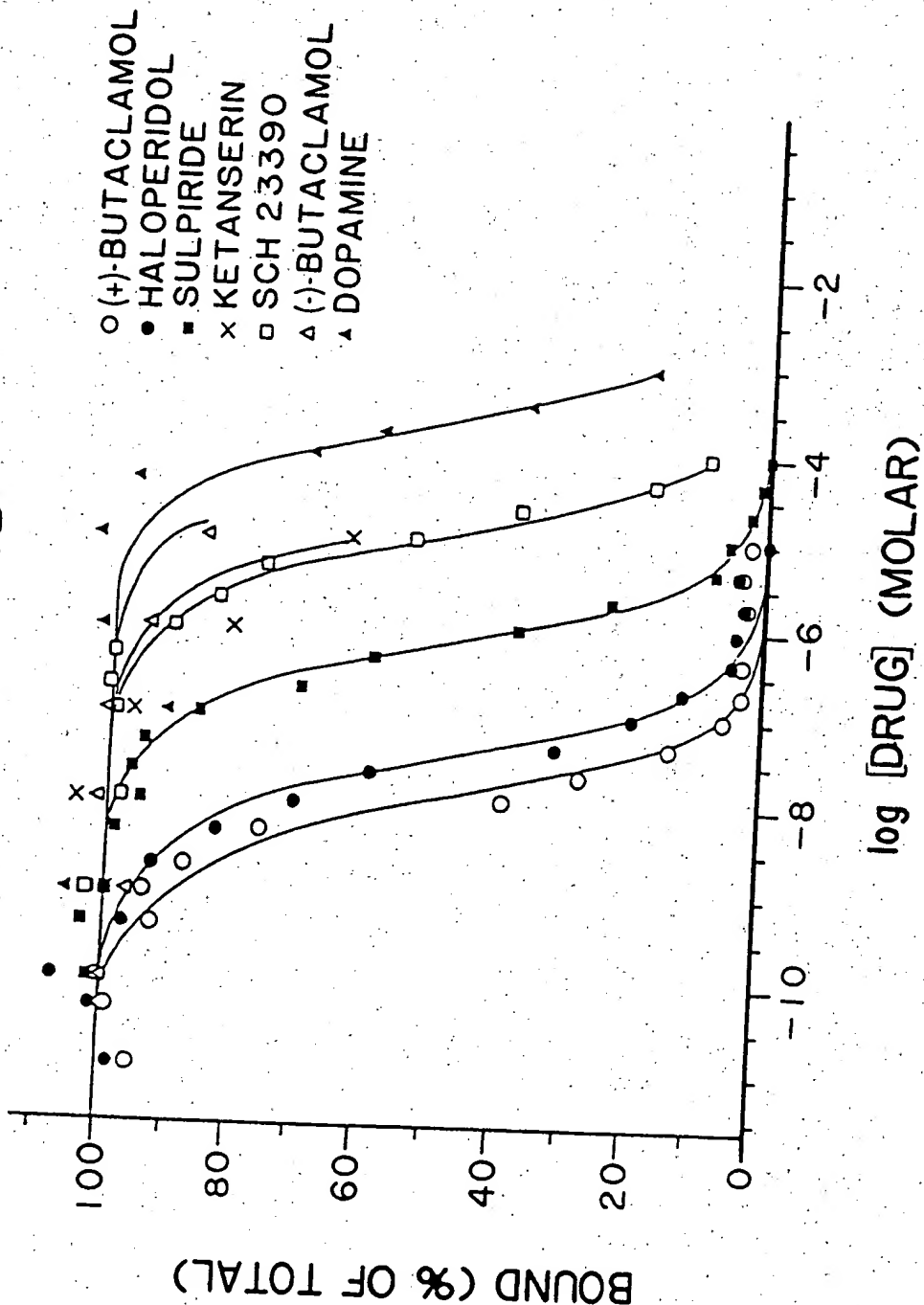


FIG. 4A-2

FIG. 4B



**DRUG** **Ki (nM)**

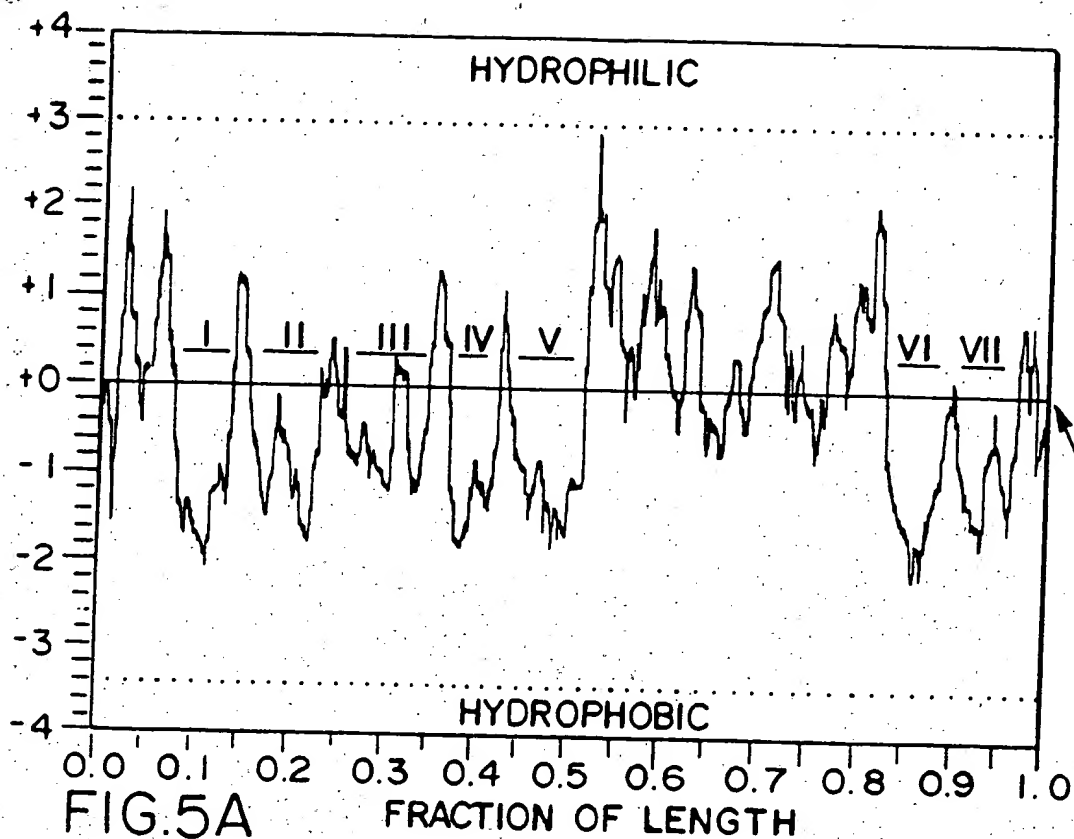
**RGB-2**

**Transformed Ltk-Cells**

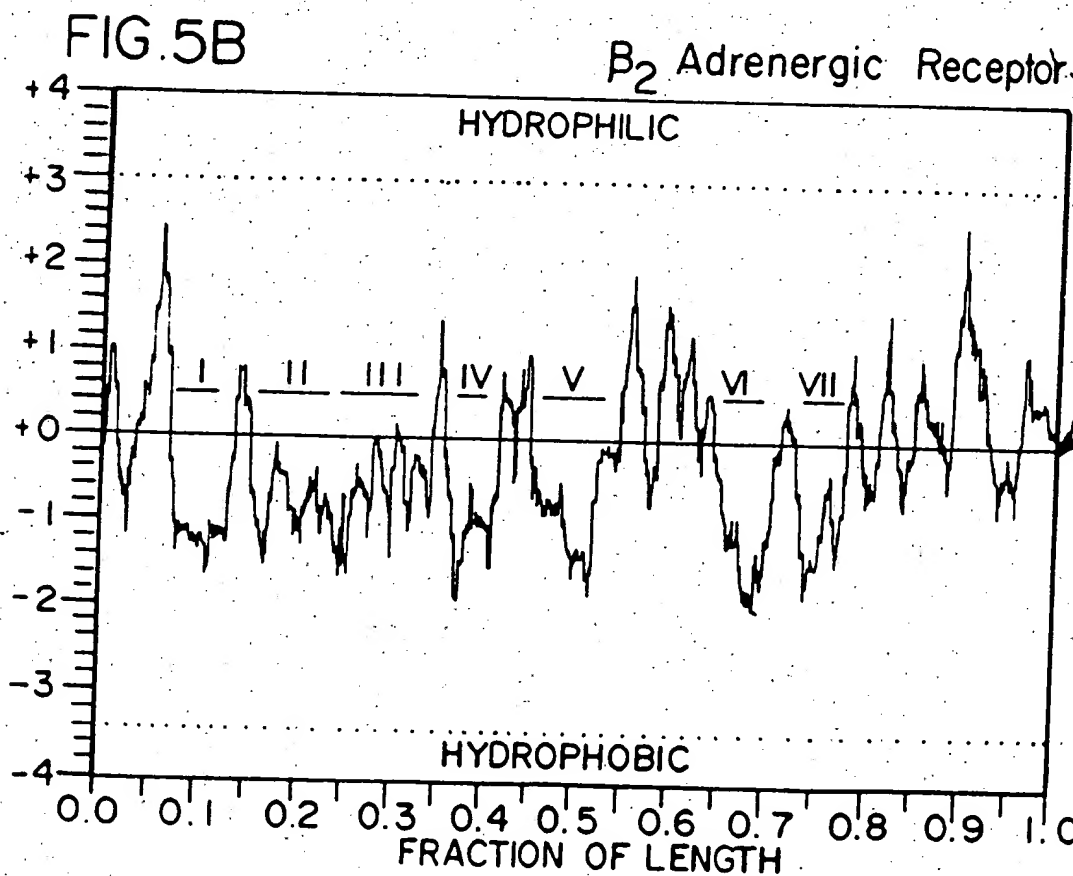
**Rat Striatum**

(+)-Butaclamol	0.83	1.0
(-)-Butaclamol	>1,000	>1,000
Haloperidol	3.0	5.3
Dopamine + GTP	17,000	6,300
Sulpiride		
high affinity	80	67 (87%)
low affinity	---	>10,000 (13%)
SCH 23390		
high affinity	---	35 (16%)
low affinity	1,000	780 (84%)
Ketanserin		
high affinity	---	27 (25%)
low affinity	>1,000	>1,000 (75%)

**FIG. 4C**

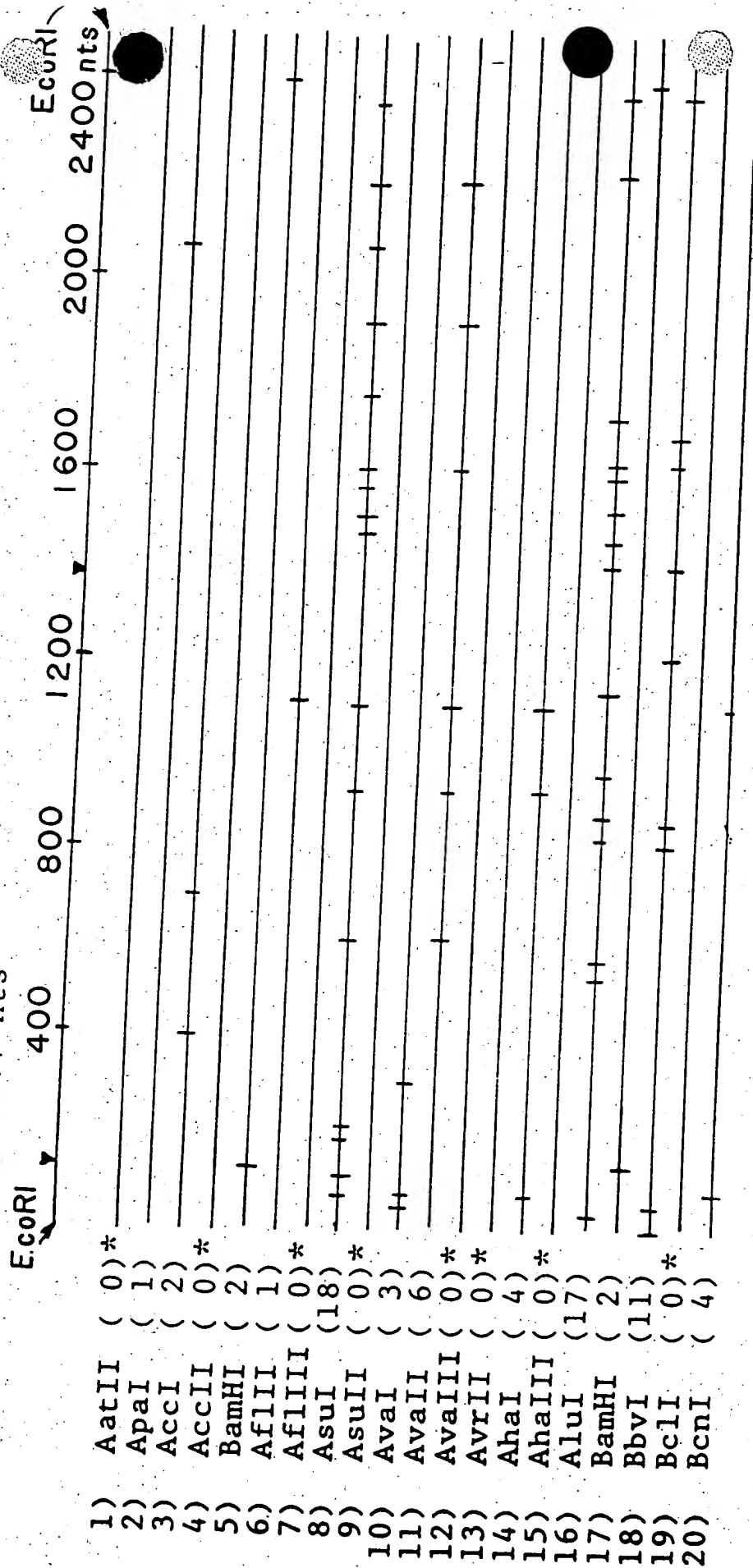


RGB-2



**FIG. 6A**

Length of DNA: 2477 nts



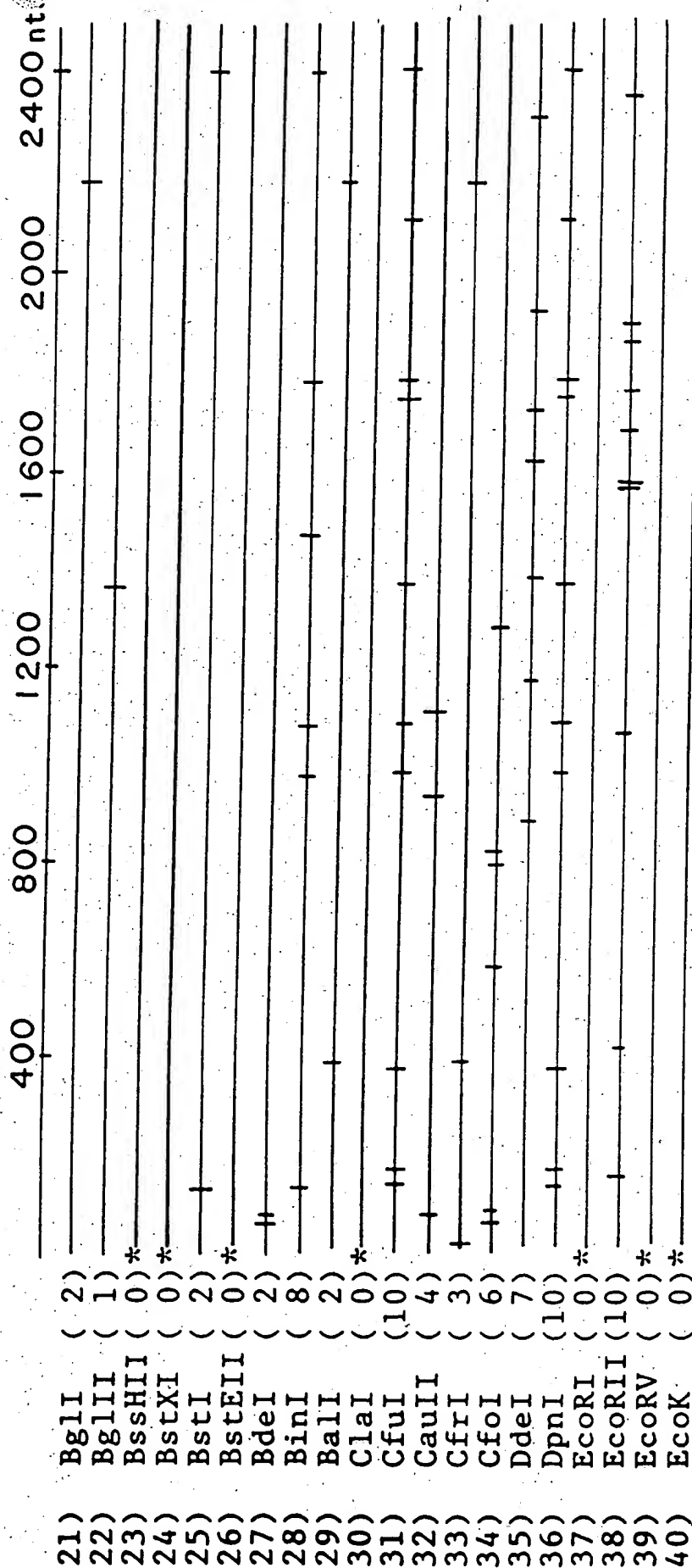


FIG. 6B

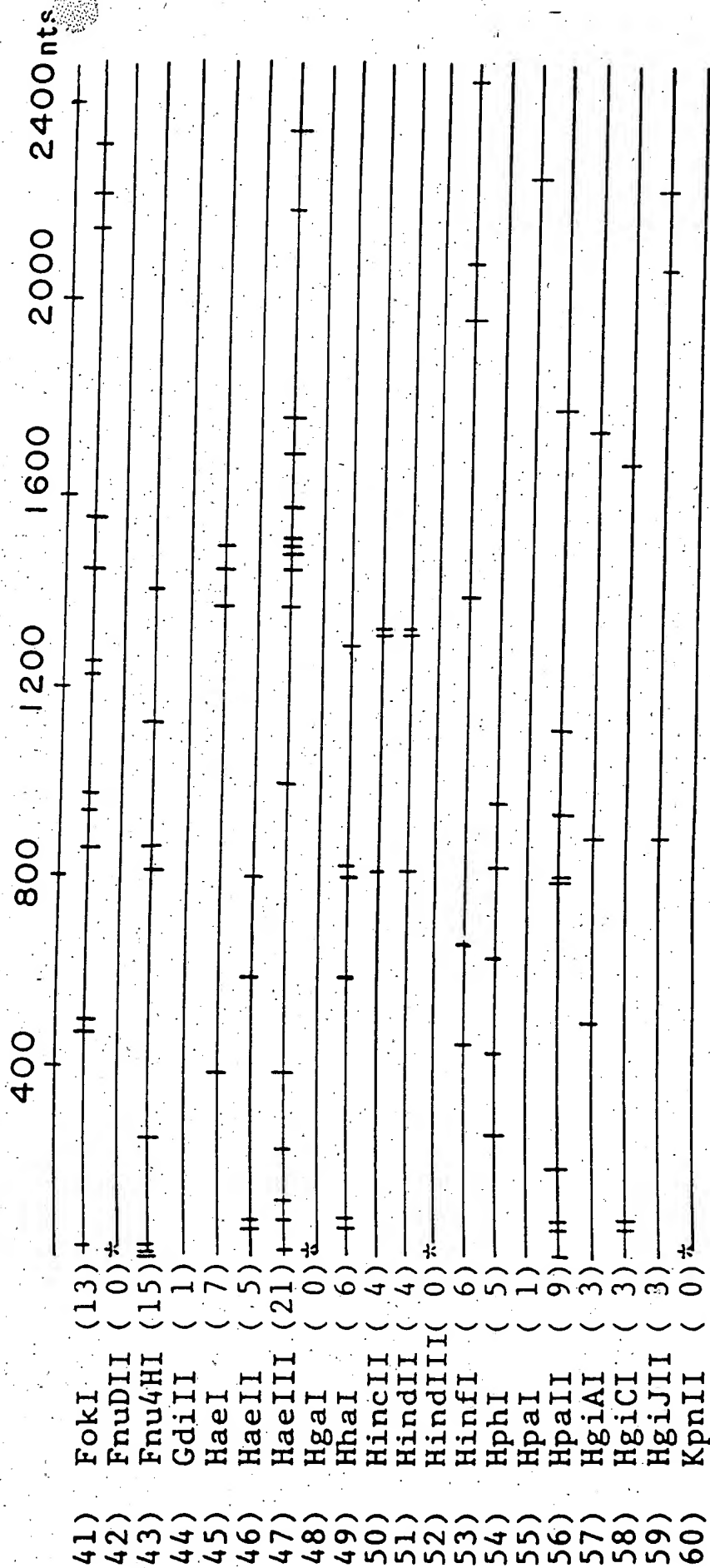


FIG. 6C

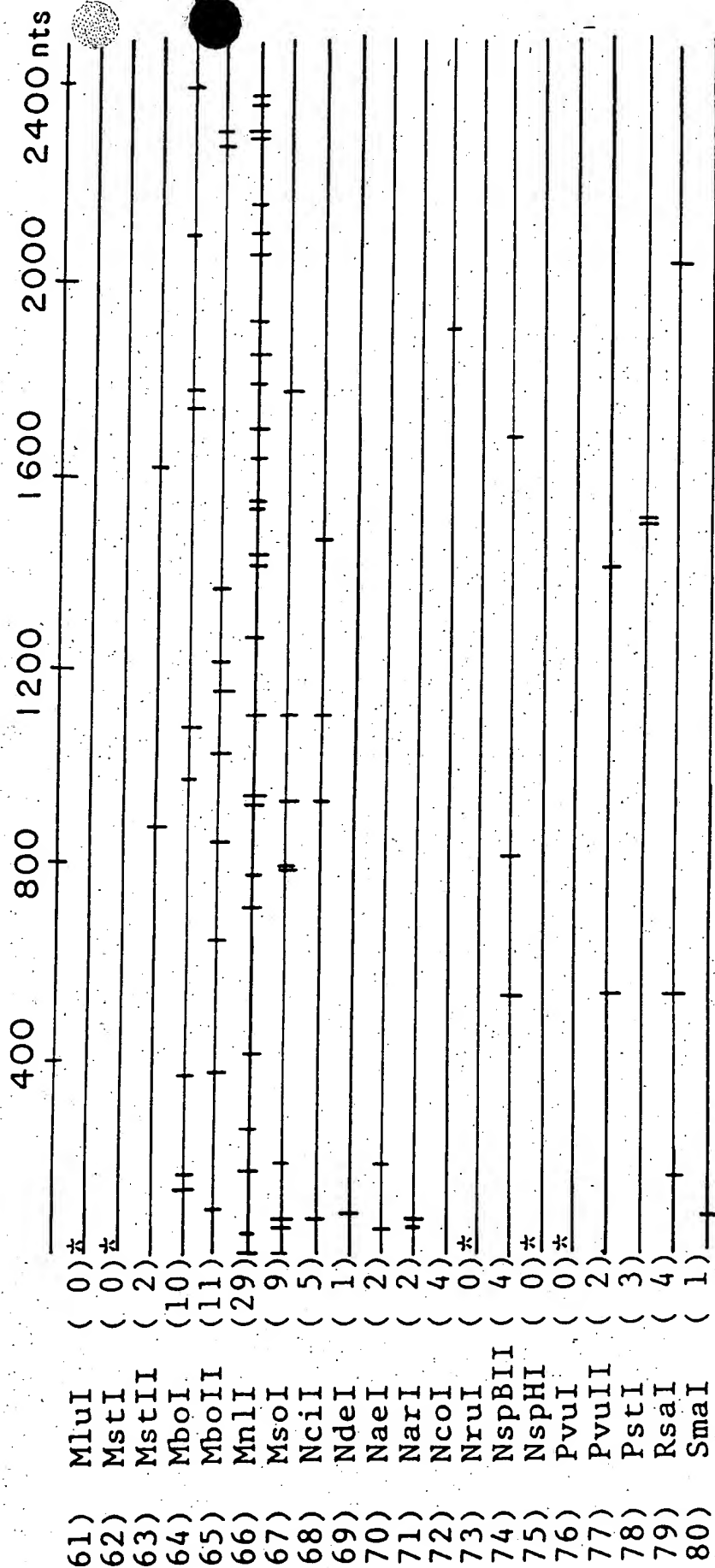


FIG. 6D



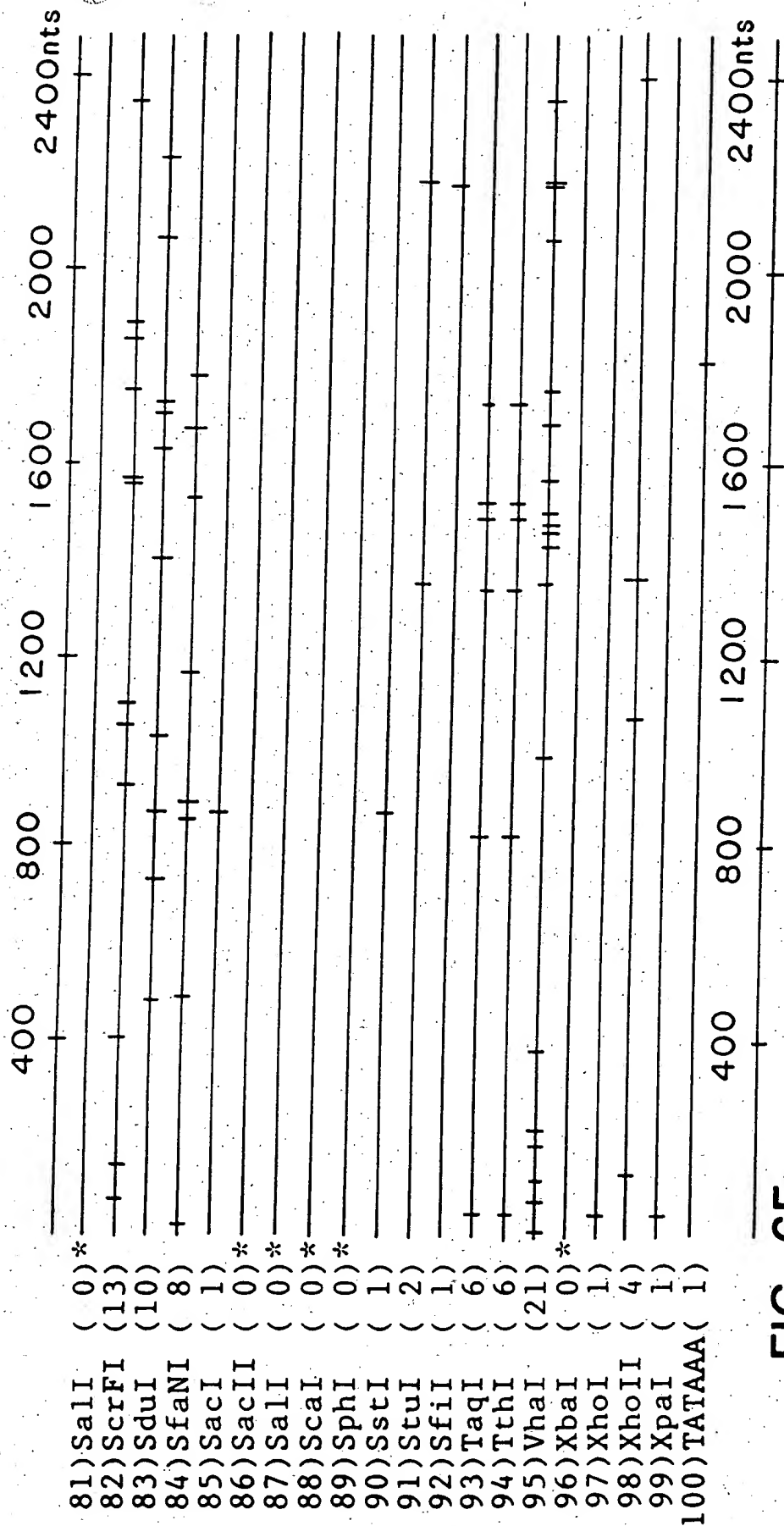


FIG. 6E

# FIG. 7A

3' GTC GGG TGG GCT CTC CTG GGC CAT GTC GGG GTA GGG TGG GTC GGT GGT GGT CGA 5' 54  
 5' CAG CCC ACC CGA GAG GAC CCG GTA CAG CCC CAT CCC ACC CAG CCA CCA CCA GCT 3'  
 Gln Pro Thr Arg Glu Asp Pro Val Gln Pro His Pro Thr Gln Pro Pro Pro Ala  
 Ser Pro Pro Glu Arg Thr Arg Tyr Ser Pro Ile Pro Pro Ser His His Gln Leu  
 Ala His Pro Arg Gly Pro Gly Thr Ala Pro Ser His Pro Ala Thr Thr Ser

81 108  
 CTC AGA GGG GCT GGG CAG GGT GGT ACC AGA GGT GTC GTG AGG GCT GTC GGG GCG  
 GAC TCT CCC CGA CCC GTC CCA CCA TGG TCT CCA CAG CAC TCC CGA CAG CCC CGC  
 Asp Ser Pro Arg Pro Val Pro Pro Trp Ser Pro Gln His Ser Arg Gln Pro Arg  
 Thr Leu Pro Asp Pro Ser His His Gly Leu His Ser Thr Pro Asp Ser Pro Ala  
 Leu Ser Pro Thr Arg Pro Thr MET Val Ser Thr Ala Leu Pro Thr Ala Pro Pro

135 162  
 GTT TGG TCT CTT CTT ACC CGT ACC GGT TTC CTG GTG GGG TTC CTA ACG GTT CTA  
 CAA ACC AGA GAA GAA TGG GCA TGC CAA AAG GAC CAC CCC AAG GAT TGC CAA GAT  
 Gln Thr Arg Glu Glu Trp Ala Cys Gln Lys Asp His Pro Lys Asp Cys Gln Asp  
 Lys Pro Glu Lys Asn Gly His Ala Lys Arg Thr Thr Pro Arg Ile Ala Lys Ile  
 Asn Gln Arg Arg MET Gly MET Pro Lys Gly Pro Pro Gln Gly Leu Pro Arg Ser

189 216  
 GAA ACT CTA GGT CTG GTA CCG GTT ACC GTT TTG GGC CTG GAG GGA GTT CTG GTA  
 CTT TGA GAT CCA GAC CAT GCC CAA TGG CAA AAC CCG GAC CTC CCT CAA GAC CAT  
 Leu . Asp Pro Asp His Ala Gln Trp Gln Asn Pro Asp Leu Pro Gln Asp His  
 Phe Glu Ile Gln Thr MET Pro Asn Gly Lys Thr Arg Thr Ser Leu Lys Thr MET

# FIG. 7B

CTC GGC ATC CTT C6A G55 GGT CGT CTT CCT CTT TCG GTG AGT CTA CGA GCG 270  
 GAG CCG TAG GAA G3T C44 CCA GCA GAA GGA GAA AGC CAC TCA GAT GCT CGC  
 Glu Pro . Glu C TT Pro Ala Glu Gly Glu Lys Lys Ala Thr Gln MET Leu Ala  
 Ser Arg Arg Lys Leu Phe Ser Arg Arg Arg Lys Pro Leu Arg Cys Ser Pro  
 Ala Val Gly Ser

GTA 5CA AGA GCC GCA CAA GTA GTA GAC GAC CGG GAA GAA GTA GTG TGT GTA 324  
 CAT 4GT TCT CCG CGT GTT CAT CAT CTG CTG GCT GCC CTT CTT CAT CAC ACA CAT  
 His T Ser Arg Arg Val His His Leu Leu Ala Ala Leu Leu His His Thr His  
 ILE Val Leu Gly Val Phe Ile Ile Cys Trp Leu Pro Phe Phe Ile Thr His Ile  
 le Phe Ser Ala Cys Ser Ser Ser Ala Gly Cys Pro Ser Ser Ser His Thr Ser

GGA CTT GTA TGT GAC ACT GAC GAC GGT GTA GGG CGG ACA GGA CAT GTC GCG GAA GTG 378  
 CCT GAA CAT ACA CTG TGA CTG CAA CAT CCC GCC TGT CCT GTA CAG CGC CTT CAC  
 Pro Glu His Thr Leu . Leu Gln His Pro Ala Cys Pro Val Gln Arg Leu His  
 Leu Asn Ile His Cys Asp Cys Asn Ile Pro Pro Val Leu Tyr Ser Ala Phe Thr  
 Thr Tyr Thr Val Thr Ala Thr Ser Arg Leu Ser Cys Thr Ala Pro Ser Arg

CAC CGA CCC GAT ACA GTT GTC GCG GCA CTT GGG GTA GTA GAT GTG GTG GAA GTT 432  
 GTG GCT GGG CTA TGT CAA CAG CGC CGT GAA CCC CAT CAT CTA CAC CAC CTT CAA  
 Val Ala Gly Leu Cys Gln Gln Arg Arg Glu Pro His His Leu His His Leu Gln  
 Trp Leu Gly Tyr Val Asn Ser Ala Val Asn Pro Ile Ile Tyr Thr Thr Phe Asn  
 Gly Trp Ala MET Ser Thr Ala Pro . Thr Pro Ser Ser Thr Pro Pro Ser Thr

459  
GTA ACT CAA GGC GTT CCG GAA GGA CTT CTA GGA GGT GAC GAC TGA GAC GAC GGA 486  
CAT TGA GTT CCG CAA GGC CTT CCT GAA GAT CCT CCA CTG CTG ACT CTG CTG CCT  
His . Val Pro Gln Gly Leu Pro Glu Asp Pro Pro Leu Leu Thr Leu Leu Pro  
Ile Glu Phe Arg Lys Ala Phe Leu Lys Ile Leu His Cys STOPLeu Cys Cys Leu  
Leu Ser Ser Ala Arg Pro Ser . Arg Ser Ser Thr Ala Asp Ser Ala Ala Cys

513  
CGG CGT GTC GTC GGA CGA AGG GTG GAG GGA CGG GTC ACC GCC GGT CGG AGT GGG 540  
GCC GCA CAG CAG CCT GCT TCC CAC CTC CCT GCC CAG TGC CGG CCA GCC TCA CCC  
Ala Ala Gln Gln Pro Ala Ser His Leu Pro Ala Gln Cys Arg Pro Ala Ser Pro  
Pro His Ser Ser Leu Leu Pro Thr Ser Leu Pro Ser Ala Gly Gln Pro His Pro  
Arg Thr Ala Ala Cys Phe Pro Pro Cys Pro Val Pro Ala Ser Leu Thr Leu

567  
AAC GCT TGG CAC TCG TCC TTC CCG ACC CAC CTA GCC GGA GAA GAT CGG GGC 594  
TTG CGA ACC GTG AGC AGG AAG GCC TGG GTG GAT CGG CCT CCT CTT CTA GCC CCG  
Leu Arg Thr Val Ser Arg Lys Ala Trp Val Asp Arg Pro Pro Leu Leu Ala Pro  
Cys Glu Pro . Ala Gly Arg Pro Gly Trp Ile Gly Leu Leu Phe . Pro Arg  
Ala Asn Arg Glu Gln Glu Gly Leu Gly Ser Ala Ser Ser Ser Ser Pro Gly

FIG. 7C

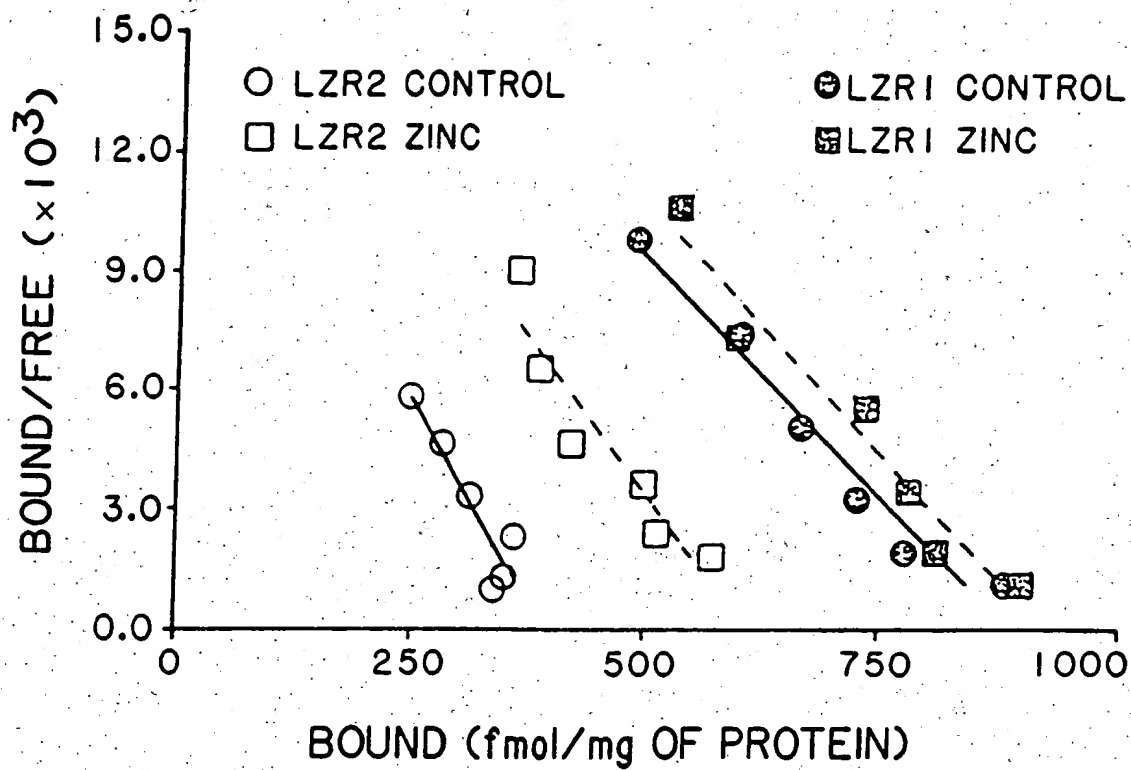
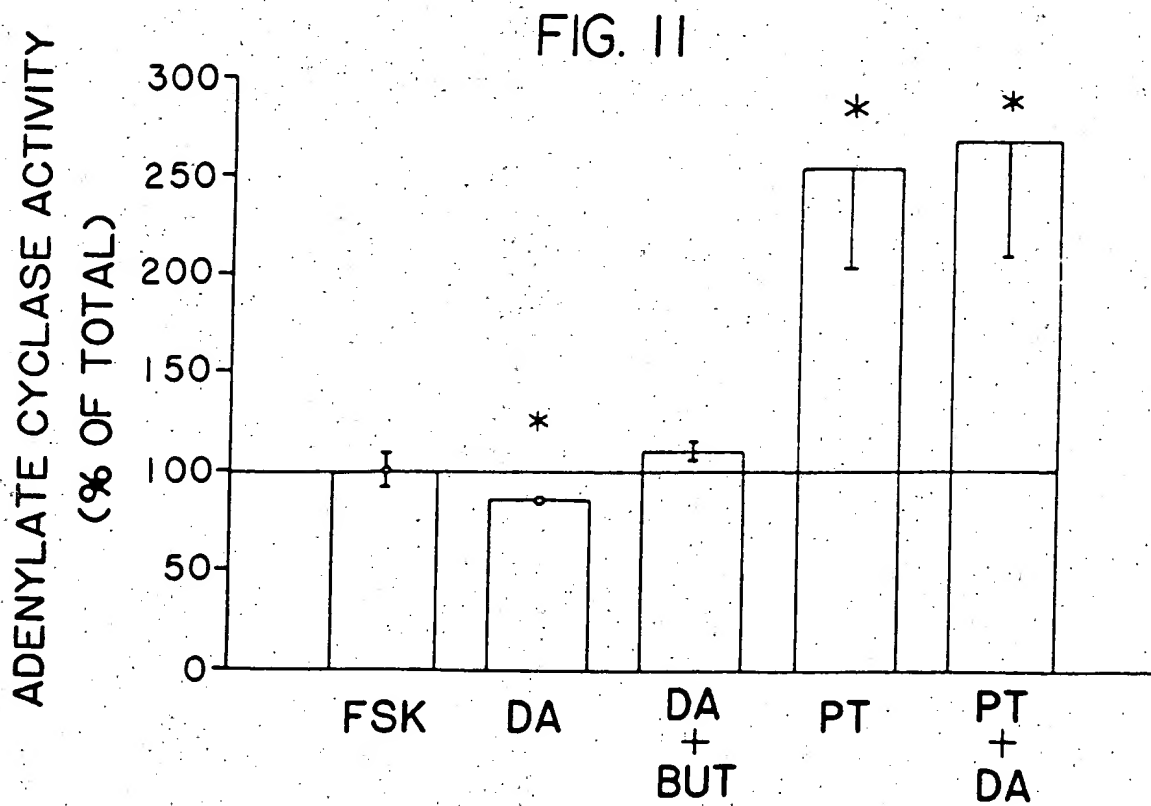


FIG. 8



101230-2344100

FIG. 9A

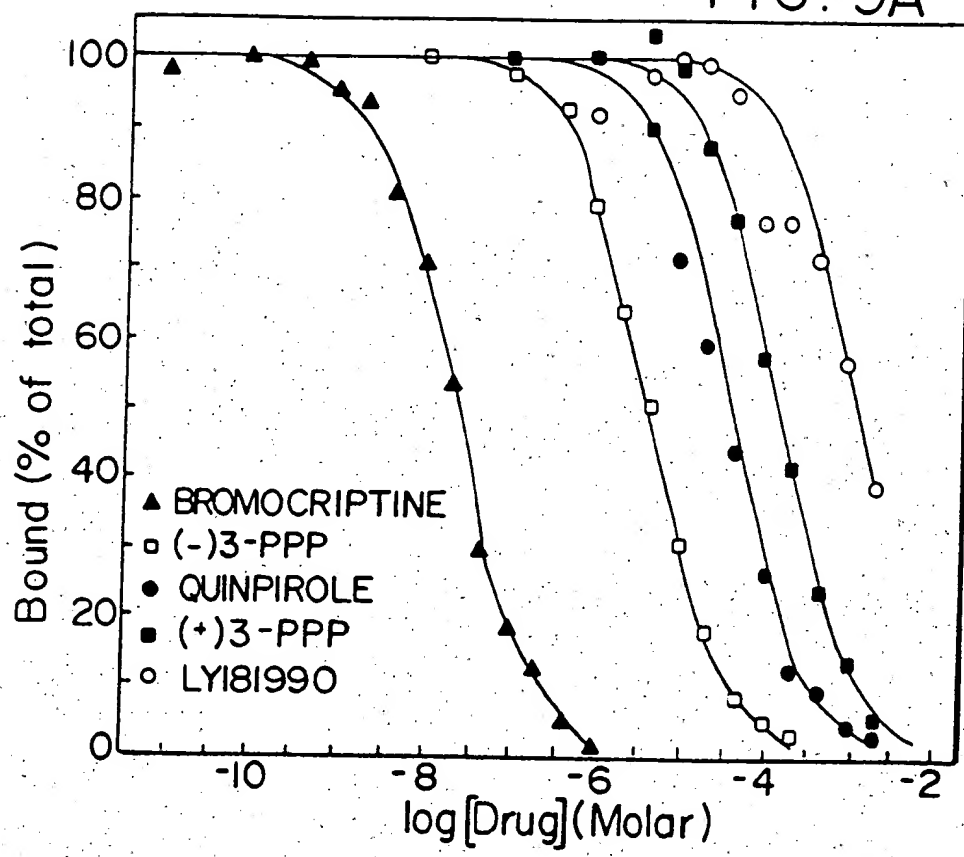
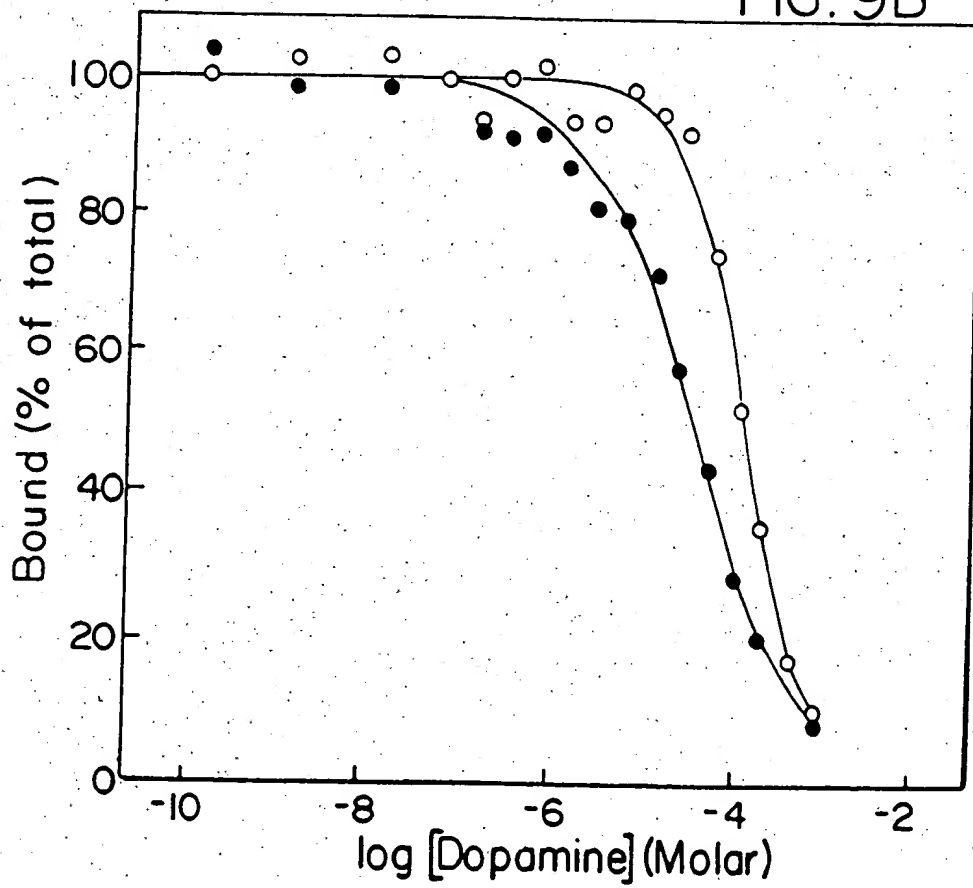


FIG. 9B



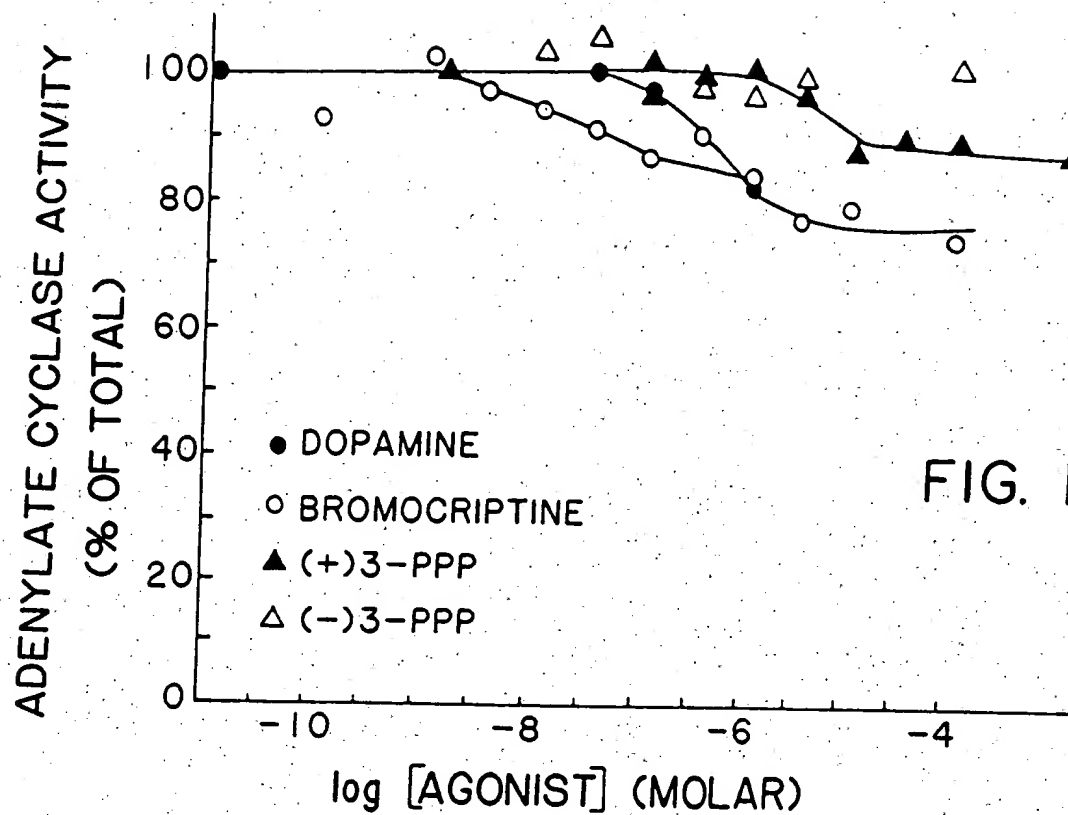


FIG. 10A

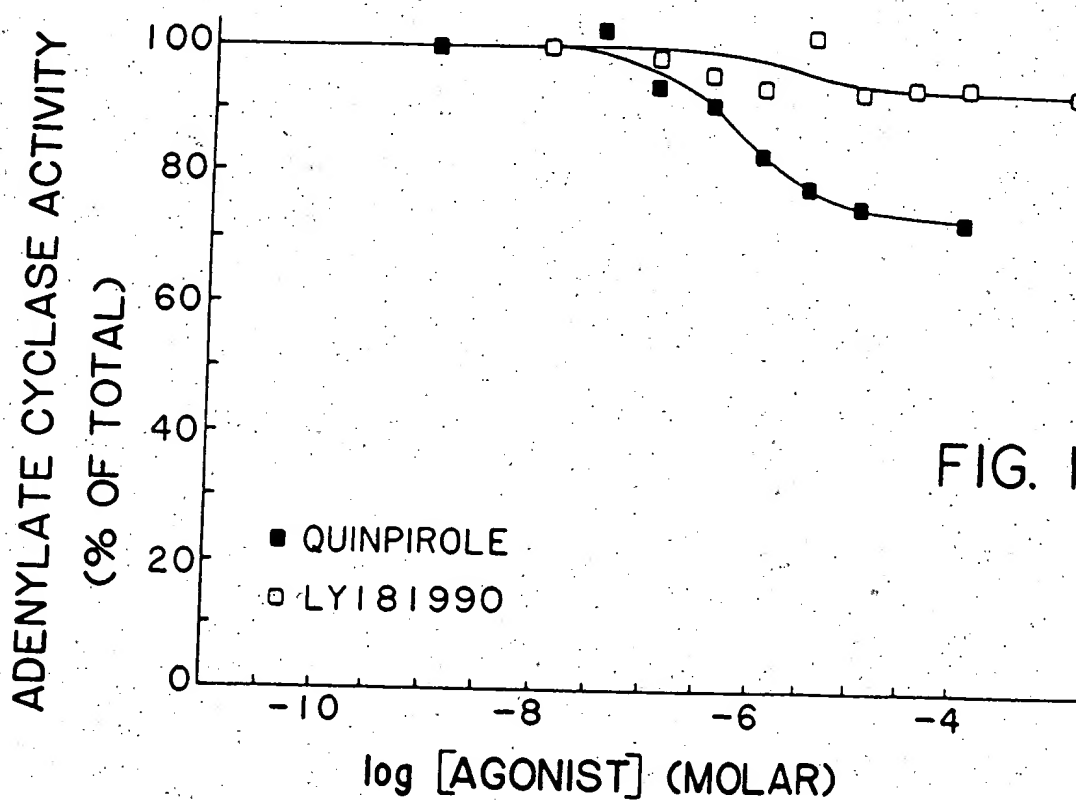


FIG. 10B

FIG. 12A

	CONTROL				+P.T.			
	BASAL	FSK	FSK+DA		BASAL	FSK	FSK+DA	
$\bar{X}$	2.1	22.6	14.3		1.7	26.7	23.1	
S.E.	0.2	2.2	2.1		0.4	2.0	0.5	
INH	—	—	41%		—	—	14%	

FIG. 12B

	CONTROL				+P.T.			
	BASAL	VIP	DA	VIP+DA	BASAL	VIP	DA	VIP+DA
$\bar{X}$	0.60	2.41	0.32	0.84	0.61	2.68	0.55	2.56
S.E.	0.02	0.31	0.02	0.13	0.09	0.08	0.03	0.25
INH	—	—	53%	71%	—	—	10%	3%

FIG. 12C

	CONTROL				+P.T.			
	BASAL	VIP	DA	VIP+DA	BASAL	VIP	DA	VIP+DA
$\bar{X}$	0.78	5.1	0.25	0.76	0.64	5.29	0.66	4.76
S.E.	0.04	0.4	0.03	0.01	0.01	0.44	0.03	0.16
INH	—	—	68%	88%	—	—	0%	12%



107280-85442660

FIG. 13B-1

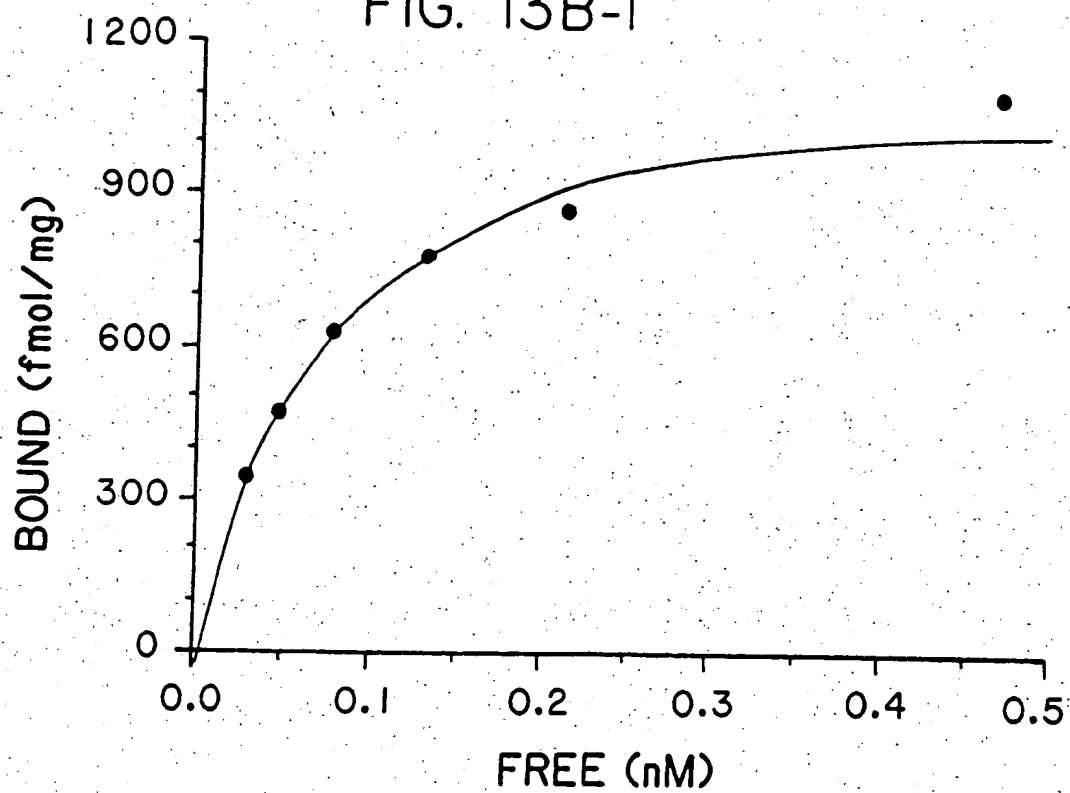
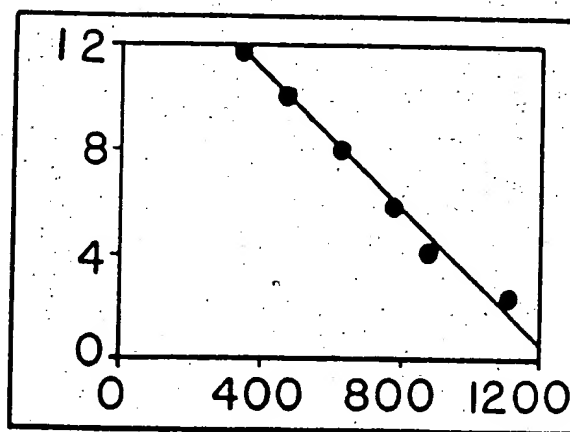


FIG. 13B-2



00000-8544660

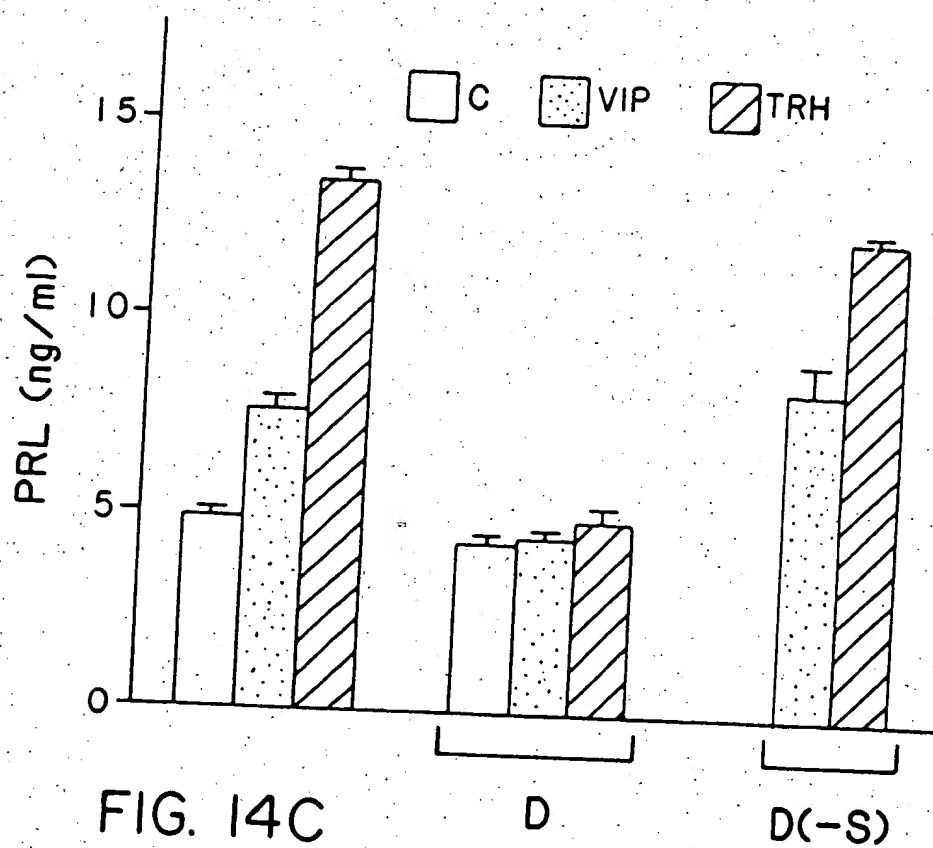
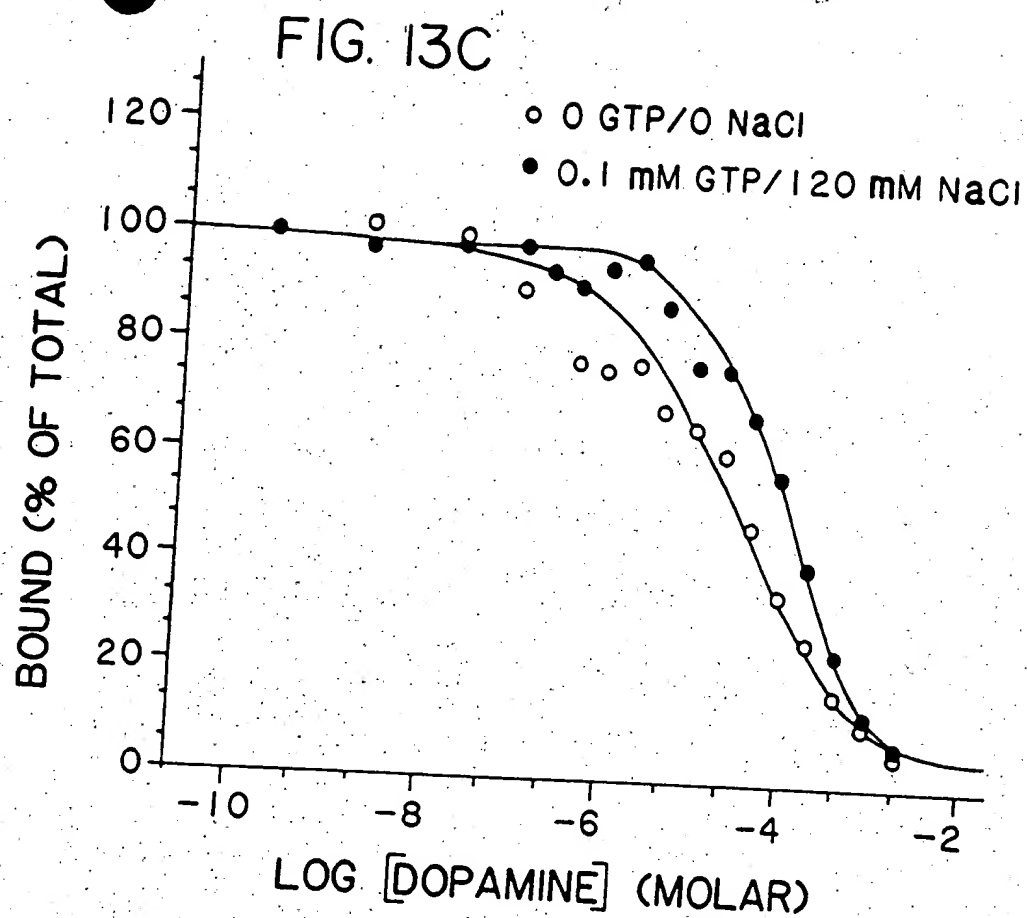


FIG.14A

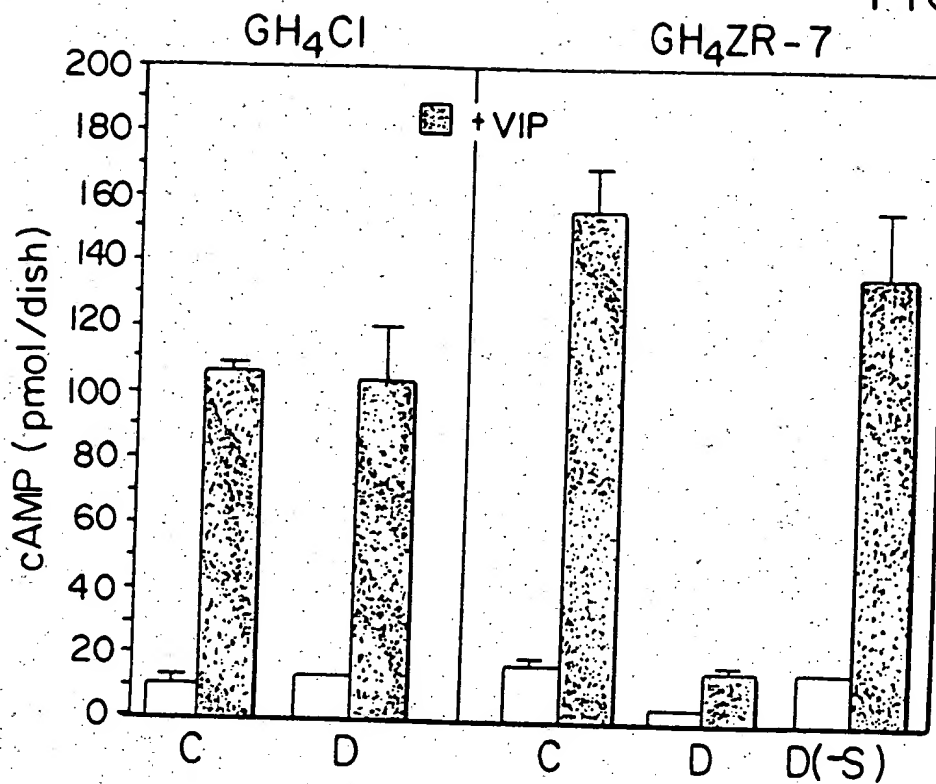
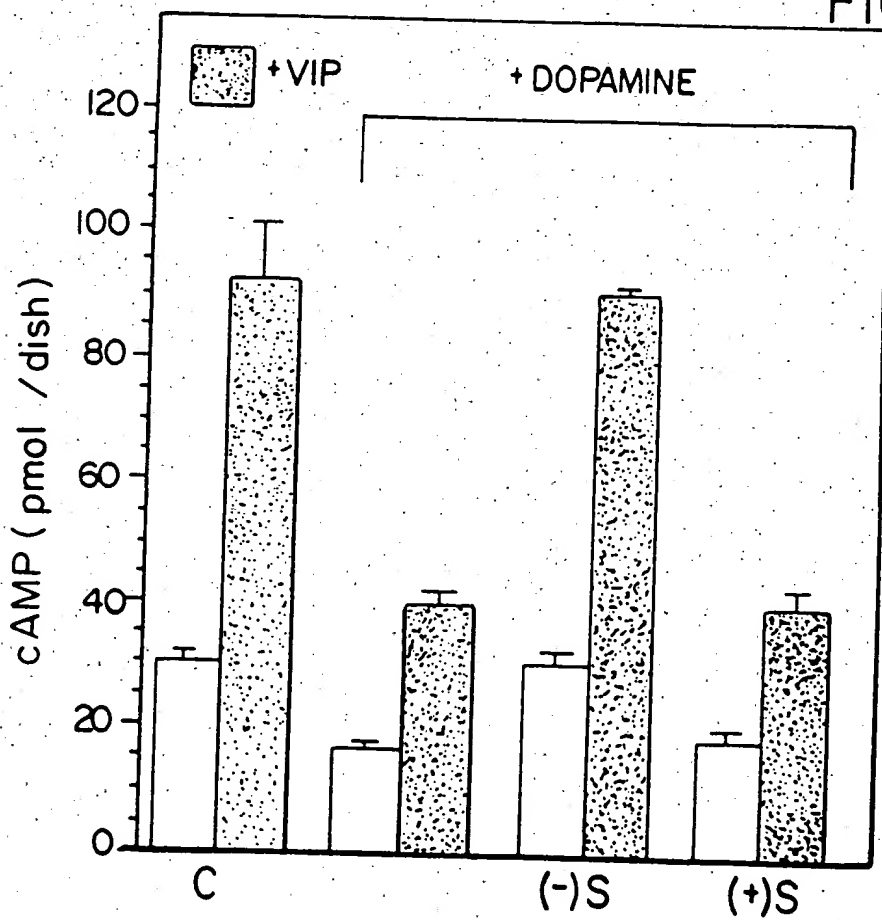


FIG.14B



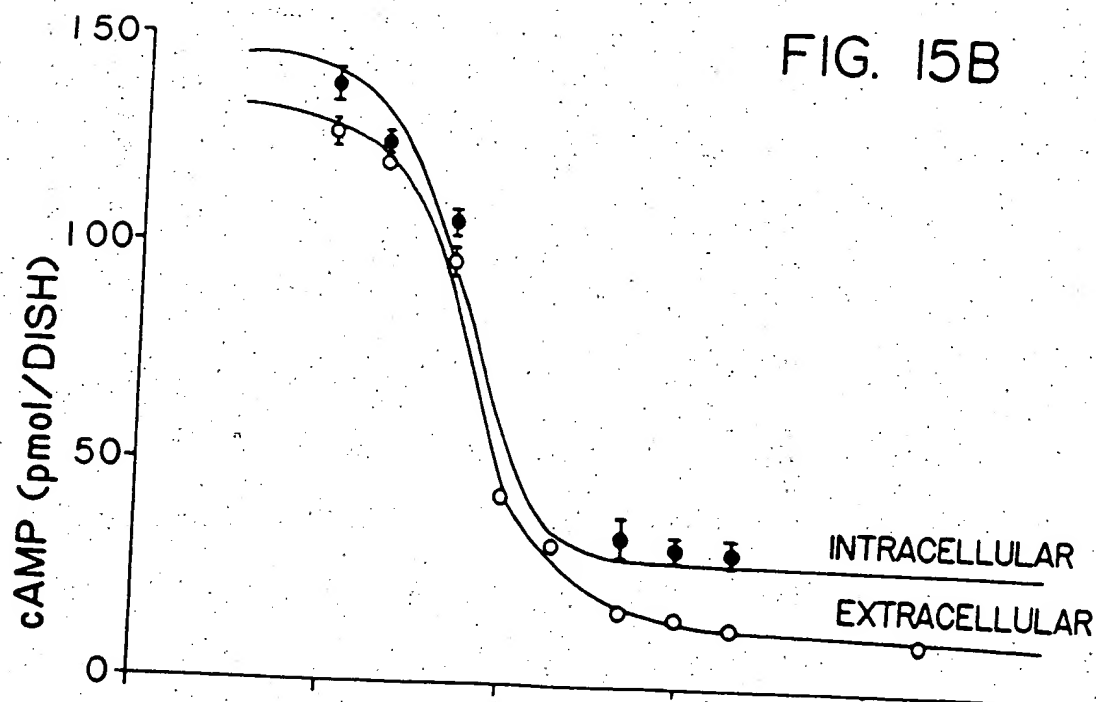
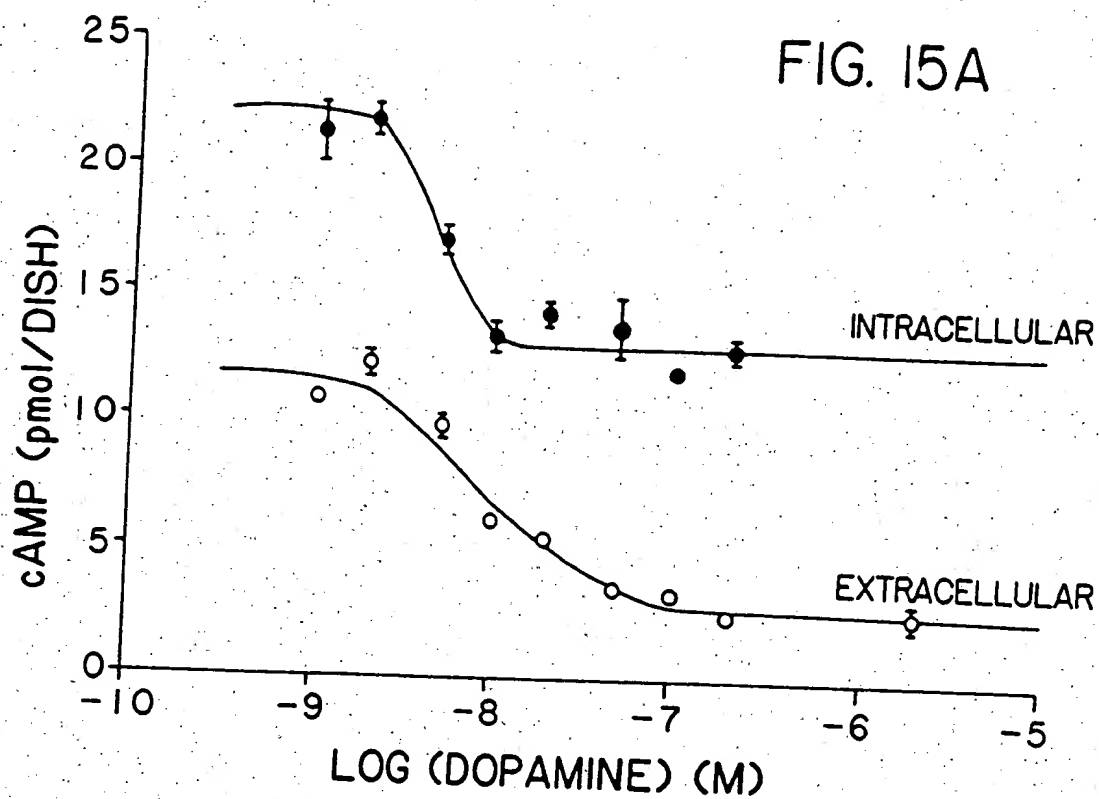


FIG. 16

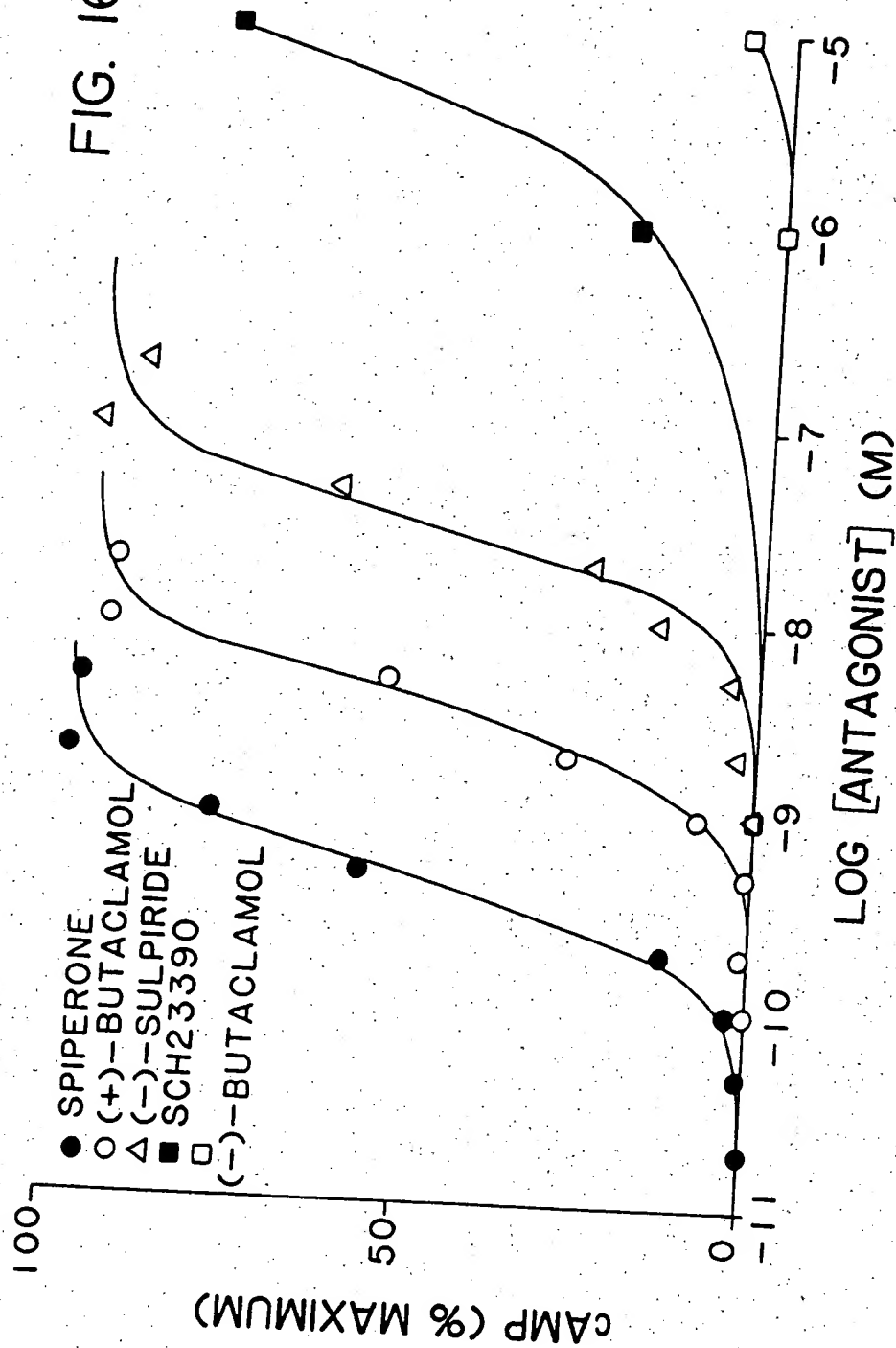


FIG.17A

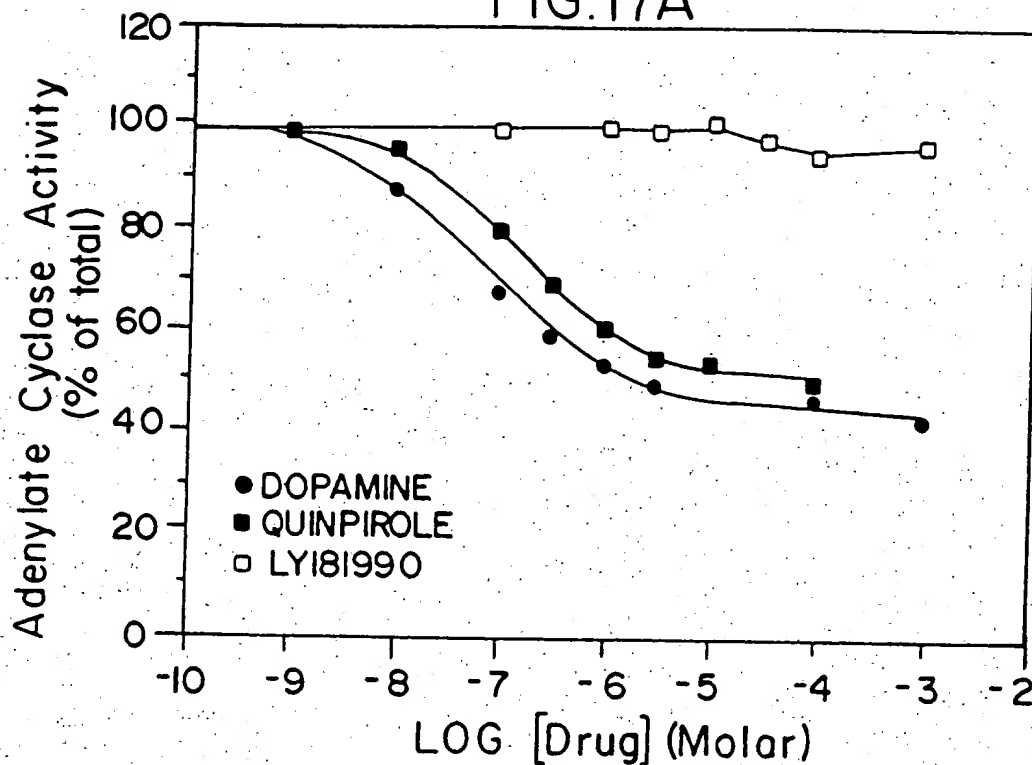
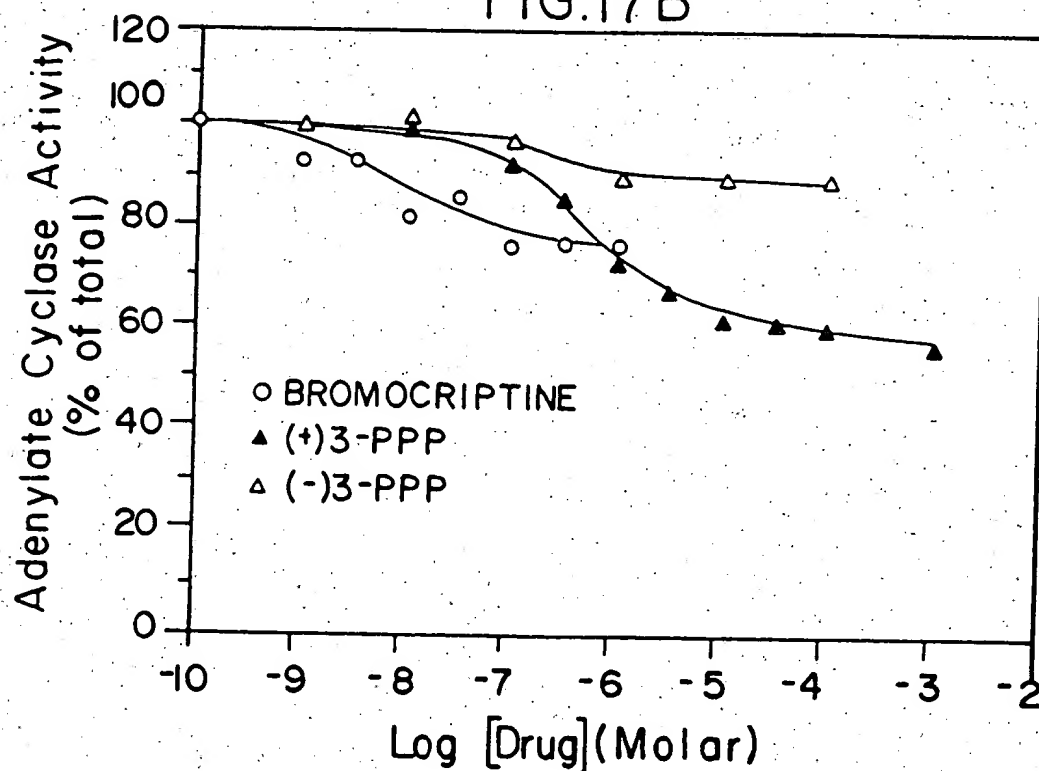


FIG.17B



-33 AGAGCCTGGCCACCCAGTGGCTCCACGCCCTG

[illegible]

CCCTTCAACGGGTCAGACGGGAAGCGGCAGACCCCACTAACTACTATGCCACACTG  
 IIIIIIII IIIIIIII IIIIIIII IIIIIIII IIIIIIII IIIIIIII IIIIIIII  
 CCCTTCAATGGGTCAGAAAGGGAAGGCAGACAGGCCCACTAACTACTATGCCATGCTG  
 Glu 120  
 MET

FIG. 18A

	1	50	60
LeuThrLeuLeuIleAlaValIleValPheGlyAsnValLeuValCysMETAlaValSer			
CTCACCCCTGCTCATCGTCTCATCGTCTTCGGCAACGTGCTGGTGCATGGCTGTGTCC			
IIIIIIII			
CTCACCCCTCATCTTATCATCGTCTTTGGCAATGTGCTGGTGCATGGCTGTATCC			
PheIle			
	70	80	
ArgGluLysAlaLeuGlnThrThrThrAsnTyrLeuIleValSerLeuAlaValAlaAsp			
CGGAGAGGCGCTGCAGACCAACCACTACCTGATCGTCAGCCTCGCAGTGCCGAC			
IIIIIIII			
CGAGAGAGGCTTTGCAGACCAACCACTACTTGATAGTCAGCCTTGCTGTGGCTGAT			240
	90	100	
LeuLeuValAlaThrLeuValMETProTrpValValTyrLeuGluValValGlyGluTrp			
CTCCTCGCCACACTGGTCAATGCCCTGGGTTGTCTACCTGGAGGTGGTAGGTAGTGG			
IIIIIIII			
CTTCTGGTGGCCACACTGGTAATGCCGTGGTGTCTACCTGGAGGTGGTGGTGGTGG			

FIG. 18B



110 120  
 LysPheSerArgIleHisCysAspIlePheValThrLeuAspValMETMETCysThrAla  
 AAATTTCAGCAGGATTCACTGTGACATCTTCGTCACTCTGGACGTCATGATGTCACGGCG  
 360  
 AAATTTCAGCAGGATTCACTGTGACATCTTTGTCACTCTGGATGTCATGATGTCACAGCA

130 140  
SerIleLeuAsnLeuCysAlaIleSerIleAspArgTyrThrAlaValAlaMETProMET  
 AGCATCCTGAACCTGTGTGCCATCAGCATCGACAGGTACACAGCTGTGGCCATGCCCCATG  
 AGCATCCTGAACCTGTGTGCCATCAGCATCGACAGGTACACAGCTGTGGCAATGCCCCATG

150 160  
 LeuTyrAsnThrArgTyrSerSerLysArgArgValThrValMETIleSerIleValTrp  
 CTGTACAATACGGCTACAGCTCCAAGCGCGGTCAACCGTCATGATCTCCATCGTCTGG  
 480  
 CTGTATAACACACGCTACAGCTCCAAGCGCGGAGTTACTGTCAATGTCATGTCCTGG  
 Ala

FIG. 18C

IV

ValLeuSerPheThrIleSerCysProLeuLeuPheGlyLeuAsnAsnAlaAspGlnAsn 170 180  
 GTCCCTGTCCTTCACCATCTCCTGCCACTCCTCTTCGGACTCAATAACGCAGACCAGAAC  
 !!!  
 GTCCCTGTCCTTCACCATCTCCTGCCACTGCTCTTCGGACTCAACAATACAGACCAGAAT  
 !!!  
 Thr

GluCysIleIleAlaAsnProAlaPheValValTyrSerSerIleValSerPheTyrVal 190 200  
 GAGTGCATCATCGCCAACCCGGCCTTCGTGGTCTACTCCTCCATCGTCTCCTTACGTG  
 !!!  
 GAGTGTATCATCGCCAACCCCTGCCTTGTGGTCTACTCCTCCATTGTCTCATTTACGTG  
 !!!  
 600

ProPheIleValThrLeuLeuValTyrIleLysIleTyrIleValLeuArgArgArg 210 220  
 CCCTTCATTGTCACCCCTGCTGTCTACATCAAGATCTACATTGTCTCCGCAGACGCCCG  
 !!!  
 CCCTTCATCGTCACTGCTGTCTATATCAAAATCTACATCGTCTCCGGAAGCGCCCG  
 !!!  
 Lys

FIG. 18D

LysArgValAsnThrLysArgSerArgAlaPheArgAlaHisLeuArgAlaProLeu	230	240
AACGAGTCAACACCAACGCAGCAGCCGAGCTTTCAGGGCCACCTGAGGGCTCCACTA		
IIIIII IIIIIIIII IIIIIIIII III IIIII I I IIIII		720
AACGGGTCAACACCAAGCGCAGCAGTCGAGCTTTCAGAGCCAACTGAAGACACCACTC		
	Asn	LysThr
* * *		
LysGlyAsnCysThrHisProGluAspMETLysLeuCysThrValIleMETLysSerAsn	250	
▼ AAGGCAACTGTACTCACCCCGAGGACATGAACTCTGCACCGTTATCATGAAGTCTAAT		
!!!		
AAG.....		
* * *		
GlySerPheProValAsnArgArgValGluAlaAlaArgArgAlaGlnGluLeuGlu	270	280
GGGAGTTTCCAGTGAACAGCGCGAGAGTGAGGCTGCCCGGCGAGCCCGAGGCTGGAG		
II IIIIIIIII IIIII IIIII IIIIIIIIIII		
.....GATGCTGCCCGCGAGCTCAGGAGCTGGAA		840
	Asp	

FIG. 18E

290 METGluMETLeuSerSerThrSerProGluArgThrArgTyrSerProIleProPro 300  
 ATGGAGATGCTCTCCAGCACCCAGCCACCCGAGAGAGACCCGGTACAGCCCATCCACCCC  
 IIIIIIIIIII IIIIIIIIIII IIIIIIIIIII IIIIIIIIIII IIIIIIIIIII III  
 ATGGAGATGCTGTCAAGCACCCAGCCCCAGAGAGAGACCCGGTATAGCCCCCATCCCTCCC

310 SerHisHisGlnLeuThrLeuProAspProSerHisHisGlyLeuHisSerThrProAsp 320  
 AGCCACCACGACTCTCCCCGACCCGTCCTCCACCATGTCTCCACAGCACTCCCGAC  
 IIIIIIIIIII IIIIIIIII IIIIIIIII IIIIIIIII IIIIIIIII IIIIIIIII  
 AGTCACCACGACTCACTCTCCCTGATCCATCCACCCACCGCCTACATAGCAACCCCTGAC  
 Asn 960

330 SerProAlaLysProGluLysAsnGlyHisAlaLys AspHisProLysIleAlaLys 339  
 AGCCCCGCCAAACCAGAGAAGATGGGCATGCCAAA... GACCACCCCAAGATTGCCAAG  
 IIIIIIIIIII IIIIIIIII IIIIIIIII IIIIIIIII IIIIIIIII IIIIIIIII  
 AGTCCTGCCAAACCAGAGAAGATGGGCACGCCCAAGATTGTCAATCCCAGGATTGCCAAG  
 IleValAsn Arg

FIG. 18F





CAGGCCGGCCAGCCTCACCCCTTGCGAACCGTGAGCAGGAAGGCTGGTGATCGGCCTC 1437

CTCTTCTTAGCCCCGGCAGGCCCTGCAGTGTTGCTTGCTCCATGCTCCTCACTGCCCG

CACACCTCACTCTGCCAGGGCAGTGCTAGTGAGCTGGGCATGGTACCAGCCCTGGGGCT 1557

GGCCCCAGCTCAGGGCAGCTCATAGAGTCCCCCTCCACCTCCAGTCCCCCTATCCTT

GGACCAAAGATGCAGCCGCCCTTCCTTGACCTTCCTCTGGGGCTCTAGGGTTGCTGGAGC 1677

CTGAGTCAGGGCCAGAGGCTGAGTTTCTCTTGTGGGGCTTGCGGTGGAGCAGGCGGT

GGGGAGAGATGGACAGTTCACACCCCTGCAAGGCCCCACAGGAGGCAAGCAAGCTCTCTGC 1797

CGAGGAGCCAGGCAACTTCAGTCCTGGGAGACCCCATGTAAATACCAGACTGCAGGTTGGA

CCCCAAGGATTCCCAAGCCAAAACCTTAGCTCCCTCCCGCACCCCGATGTGGACCTCTA 1917

FIG. 18I

CTTCCAGGCTAGTCCGGACCCACCTCACCCCGTTACAGCTCCCCAAGTGGTTCCACAT

GCTCTGAGAAGAGAGCCCTCATCTTGAAGGCCACAGAGGCTCTATGGGAGAGGAACT 2037

CCTTGGCCTAGCCCACCCCTGCTGCCCTTCTGACGGCCCTGCAATGTATCCCTTCTCACAGC

ACATGCTGGCCAGCCTGGGGCCTGGCAGGGAGGTCAGGCCCTGGAACCTATCTGGGCCT 2157

GGGCTAGGACATCAGAGGTTCTTTGAGGAGTCCCTCTGCCACACTCTGACGCAAAACC

ACTTTCCTTTTCTATTCCCTTCTGGCCCTTTCCTCTCTCCTGTTTCCCTTCCCTTCCACTGC 2277

CTCTGCCCTTAGAGGAGCCACGGCTAAGAGGCTGCTGAAACCATCTGGCCTGGCCTGGC

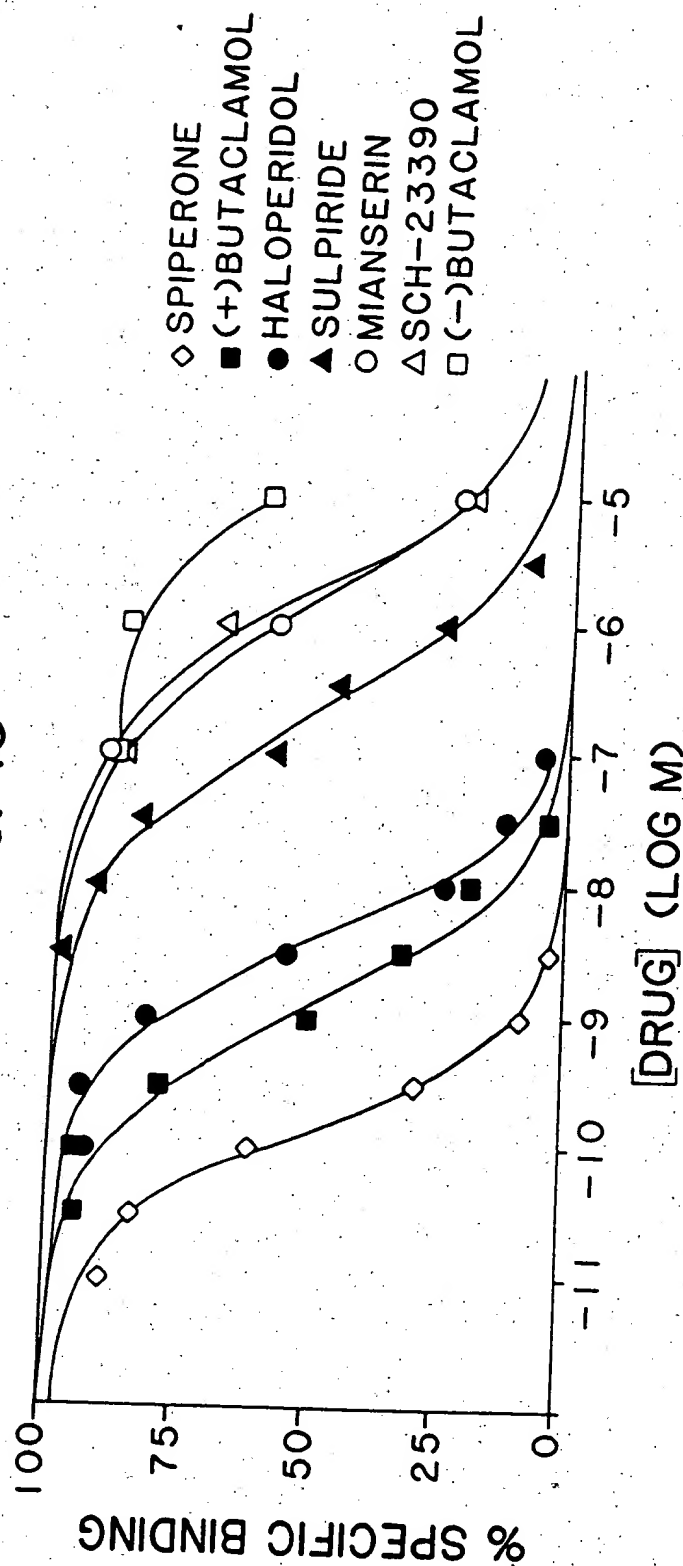
CCTGCCCTGAGGAAGGAGGGCAAGCTGCAGCTTGGGAGAGCCCTGGGGCCTAGACTCTG 2397

TAACATCACTATCCGATGCACCAAACTAATAAACTTTGACGAGTCACCTTC (A)<sub>n</sub> 2449

FIG. 18J



FIG. 19



1 2 3 4

kb

—12.0

— 6.0

— 4.0

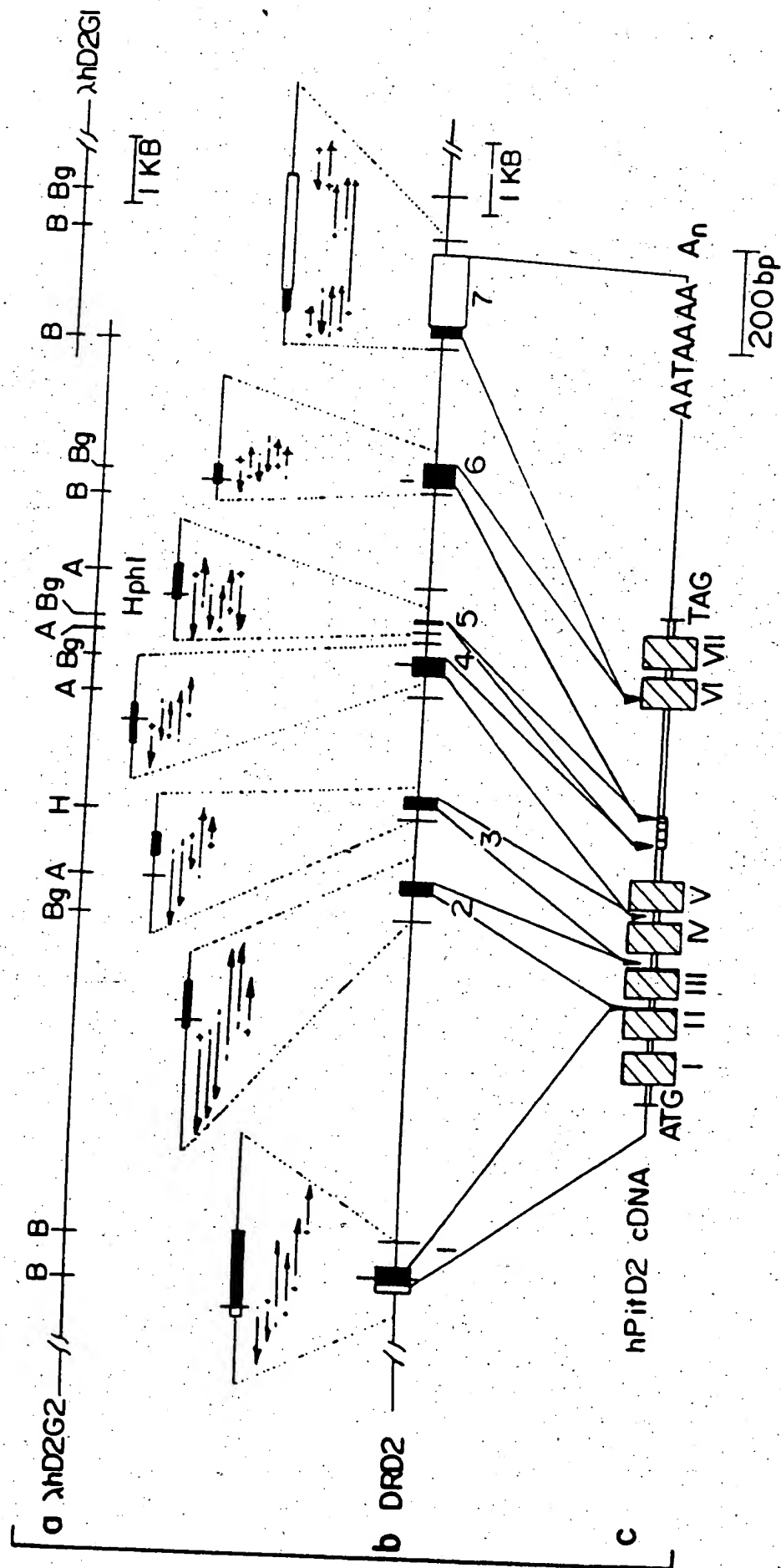
— 2.0

— 1.6

— 1.0

FIG. 20

FIG. 21



DRUG	HUMAN D <sub>2</sub>	RAT D <sub>2</sub>	RAT STRIATUM
SPIPERONE	0.125	0.35	0.56
(+) BUTACLAMOL	0.94	1.2	1.6
HALOPERIDOL	2.4	5.1	5.8
SULPIRIDE	206	160	205
MIANSERIN (5-HT)	2685	4300	4600
SCH 23390 (DI)	2145	2500	3300
(+) BUTACLAMOL	>10,000	>10,000	>10,000
Kd [ <sup>3</sup> H] DOMPERIDONE	0.74	0.40	0.40

FIG. 22

FIG. 23

285 <sup>1</sup>	286
exon1...GGAGgtagtg...intron1...tccccagGTGG...exon2	
395	396
exon2...ACAGgtgagcc...intron2...cttgacgGTAC...exon3	
532	533
exon3...GCAGgtacatt...intron3...ccccccagACCA...exon4	
723	724
exon4...AAAGgtctcaa...intron4...tccacagGGCA...exon5	
810	811
exon5...AGTGgtaagtg...intron5...ggtagcagGAGG...exon6	
1138	1139
exon6...CTCGgtgagtc...intron6...ccccccagCGGT...exon7	

<sup>1</sup>Numbering begins with A of the putative initiator methionine codon (see Fig. 18)